

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 19:53:00 ; Search time 96 Seconds
(without alignments)
1336.214 Million cell u

Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESISMGSPLSSETCLPN.....ALVLPSIVILDLLQLCRY

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:
1: geneseqp1980s:/*
2: geneseqp1990s:/*
3: geneseqp2000s:/*
4: geneseqp2001s:/*
5: geneseqp2002s:/*
6: geneseqp2003as:/*
7: geneseqp2003bs:/*
8: geneseqp2004s:/*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB ID	Description
1	2351	100.0	454	AAE02781
2	2351	100.0	454	AAU10188
3	2351	100.0	454	ABG61933
4	2351	100.0	454	AAU76538
5	2351	100.0	454	AAU80190
6	2351	100.0	454	ABU08893
7	2348	99.9	454	ADB65001
8	2294	97.6	490	ADE28951
9	2294	97.6	490	ABU63312
10	2290	97.4	490	AAU10187
11	2036	86.6	419	AAU10189
12	1972.5	83.9	576	ABG12306
13	1972.5	83.9	1273	4 ABG00113
14	1738	73.9	450	AAE02841
15	1364.5	58.0	1082	5 ABP62883
16	1316	56.0	488	4 AAB49483
17	1316	56.0	526	5 ABB83365
18	1272	54.1	488	4 AAB85775
19	1272	54.1	488	5 ABB83366
20	1269	54.0	488	4 AAB93224
21	1269	54.0	488	4 AAU04564
22	1269	54.0	488	4 AAU10220
23	1269	54.0	488	6 ABU60864
24	1245.5	53.0	487	4 AAB49481
25	1088	46.3	459	4 AAB74715

		RESULT 1
	ID	AAE02781
XX		AAE02781 standard; protein; 454 AA.
AC		AAE02781;
XX		
DT		06-AUG-2001 (first entry)
XX		
DE		Human six transmembrane epithelial antigen of prostate (STEAP)-2 protein.
KW		Human; cytostatic; antiproliferative; vaccine; gene therapy;
KW		six transmembrane epithelial antigen of the prostate-2; STEAP-2;
KW		chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian;
KW		pancreatic.
XX		
OS		Homo sapiens.
XX		
FH		Key
PT		Location/Qualifiers
PT		Region 100..108
PT		/label=HLA-A2_binding_peptide #5
PT		Region 153..165
PT		/label=Immunogenic_peptide #1
FT		Domain 207..228
FT		/label=Transmembrane_domain #1
FT		Region 227..235
FT		/label=HLA-A2_binding_peptide #1
FT		Domain 255..277
FT		/label=Transmembrane_domain #2
FT		Domain 304..325
FT		/label=Transmembrane_domain #3
FT		Region 306..314
FT		/label=HLA-A2_binding_peptide #4
FT		Region 307..315
FT		/label=HLA-A2_binding_peptide #3
FT		Region 345..358
FT		/label=Immunogenic_peptide #2
FT		Domain 359..381
FT		/label=Transmembrane_domain #4
FT		Domain 393..415
FT		/label=Transmembrane_domain #5
FT		Region 402..410
FT		/label=HLA-A2_binding_peptide #2
FT		Domain 428..450
FT		/label=Transmembrane_domain #6
PN		WO200140276-A2
XX		
PD		07-JUN-2001.

XX
PF 06-DEC-2000; 2000WO-US033040.
XX
PR 06-DEC-1999; 99US-00455486.
XX
PA (UROG-) UROGENESIS INC.
XX
PI Afar DEH, Hubert RS, Raitano AB, Saffran DC, Mitchell SC;
PI Paris M, Jakobovits A;
XX
DR WPI; 2001-367804/38.
DR N-PSDB; AAD07072.

PT New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating cancer.
XX
PT Claim 1; Fig 9A-9C; 187pp; English.

CC The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP, or in a patient, comprises administering a vaccine composition to the patient. Treating a patient that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly. Note: This sequence is stated to be the same as that being shown as SEQ ID NO:8 (AAE02841) in sequence listing of the specification. However both the sequences differ at several positions
XX
SQ Sequence 454 AA;

Query Match 100.0%; Score 2351; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 5e-245;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGGSPKSLSETCLPNCINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
Db 1 MESISMGGSPKSLSETCLPNCINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHRHYTSWLDLRHLIVGKILIDSNNM 120
Db 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHRHYTSWLDLRHLIVGKILIDSNNM 120
QY 121 RINQYPPESNAEYLASFPDSLIVKGFNVSAWALQLGPKDASRQVWICSNNIQARQVIE 180
Db 121 RINQYPPESNAEYLASFPDSLIVKGFNVSAWALQLGPKDASRQVWICSNNIQARQVIE 180
QY 181 LARQNLNFIPIRIDGSASSAREIENLPLRLFTLWRGPVVVAISLATEFLYSFVRDVHPYA 240
Db 181 LARQNLNFIPIRIDGSASSAREIENLPLRLFTLWRGPVVVAISLATEFLYSFVRDVHPYA 240
QY 241 RNQQSDFYKIPTEIWNKTRPIVATILLSLVYLAGLMAAYOLYYGKTYRKRFRPPWLETWLO 300
Db 241 RNQQSDFYKIPTEIWNKTRPIVATILLSLVYLAGLMAAYOLYYGKTYRKRFRPPWLETWLO 300
QY 301 CRKQOLGLISFFFAMNHVAVSLSLCLPMRRSERYLFLNMAYQCVHANTENSNEEEVWRIEMY 360
Db 301 CRKQOLGLISFFFAMNHVAVSLSLCLPMRRSERYLFLNMAYQCVHANTENSNEEEVWRIEMY 360
QY 361 ISFGIMMSIGLLSLLAVTSIPSVSNALNWREFSFTOSTGYVALLISTFHVLYGWKRAFE 420
Db 361 ISFGIMMSIGLLSLLAVTSIPSVSNALNWREFSFTOSTGYVALLISTFHVLYGWKRAFE 420
QY 421 EYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454

XX
PT Human ORF2 of Six-Transmembrane Protein of Prostate 1.
DE Human ORF2 of Six-Transmembrane Protein of Prostate 1; STMPL; prostate cancer; KW Human; Six-Transmembrane Protein of Prostate 1; STMPL; prostate cancer; KW benign prostatic hyperplasia; acute prostatitis; testicular cancer; KW cryptorchidism; testicular disorder; proliferative disorder; lymphoma; KW leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ORF2.
XX
OS Homo sapiens.
XX
WO200172962-A2.
XX
PD 04-OCT-2001.
XX
PP 23-MAR-2001; 2001WO-US009410.
XX
PR 24-MAR-2000; 2000US-0191929P.
XX
(SAAT/) SAATCIOGLU F.
XX
PI Saatcioglu F;
XX
WPI; 2001-662926/76.
DR N-PSDB; AAS15810, AAS15811.
XX
PT New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises PT prostate-specific or testis-specific nucleic acids.
XX
PS Claim 1; Fig 4H; 114pp; English.

CC The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that modulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostate hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. The present sequence is prostate specific protein, Six-Transmembrane protein of prostate 1, STMPL, ORF2
XX
SQ Sequence 454 AA;

Query Match 100.0%; Score 2351; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 5e-245;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGGSPKSLSETCLPNCINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
1 MESISMGGSPKSLSETCLPNCINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHRHYTSWLDLRHLIVGKILIDSNNM 120
61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHRHYTSWLDLRHLIVGKILIDSNNM 120

QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE	180	CC	associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The
Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE	180	CC	prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.
QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA	240	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA	240	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ	300	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ	300	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY	360	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY	360	CC	ABG61800-ABG61944 represent prostate cancer-associated proteins
RESULT 3			SQ	Sequence 454 AA:
ID	ABG61933		Query Match	100.0%; Score 2351; DB 5; Length 454;
XX			Best Local Similarity	100.0%; Pred. No. 5e-245;
AC	ABG61933;		Matches	454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX			Db	1 MESISMGMSPKLSSETCLPQNGINGIKDARKVTVGVIGSGDFAKSLTIRLRCGYHVG 60
DT	15-AUG-2002 (first entry)		QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
DE	Prostate cancer-associated protein #134.		QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.			QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
OS			Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
PN	WO200230268-A2.		Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			QY	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PD	18-APR-2002.		Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
PF	12-OCT-2001; 2001WO-US032045.		Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
PR	13-OCT-2000; 2000US-00687576.		Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
PR	08-DEC-2000; 2000US-00733288.		QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
PR	08-DEC-2000; 2000US-00733288.		Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
PR	08-DEC-2000; 2000US-00733288.		QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PR	08-DEC-2000; 2000US-00733288.		Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PR	24-JAN-2001; 2001US-0263957P.		QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
PR	16-MAR-2001; 2001US-0276791P.		Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
PR	16-MAR-2001; 2001US-0276888P.		QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
PR	06-APR-2001; 2001US-0281922P.		Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
PR	24-APR-2001; 2001US-0286214P.		QY	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PR	30-APR-2001; 2001US-00847046.		Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PR	04-MAY-2001; 2001US-0288589P.		QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
PA	(EOSB-) EOS BIOTECHNOLOGY INC.		Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
PT	Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;		Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
DR	N-PSDB; ABK92252.		Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PT	Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue.		Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
PT	The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-		QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
CC			Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
CC			QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
CC			Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			QY	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			QY	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			QY	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			QY	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			Db	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFWLQ
XX			QY	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
XX			Db	301 CRKQOLGLISFFFAMVHVAYSLCLPMRRSERYLFNMAAYQVHANIENSNEEVWRIEMY
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XX			Db	361 ISFGIMSLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
XX			Db	421 EYVYRFYTPPNFVLVALVLSIVLDLQLCRYD 454
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XX			Db	61 RNPKEASEEFFPHVVDVTHEDALTNTNIFVAIHEREHTSLWDLRHLLVGKILIDVSNNM 120
XX			QY	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			Db	121 RINOYPESNAEYLASLFPDSLIVKGFNVSAWALQLGPKDASRQVICSNNIQARQQVIE
XX			QY	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			Db	181 LARQINFPIDLGSLSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA
XX			QY	241 RNQOSDFYKIPIEVNKTLPIVAITLSSLVLAGLLAAAYOLYYGTYRRFPFW

FT Region
 FT /note= "N-myristoylation site"
 FT /note= "cAMP- and cGMP-dependent protein kinase
 phosphorylation site"
 FT 34. .39
 FT /note= "N-myristoylation site"
 FT Modified-site
 FT 193. .198
 FT /note= "N-myristoylation site"
 FT Domain
 FT 210. .230
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 FT 256. .259
 FT /note= "Asn is N-glycosylated"
 FT 257. .277
 FT Domain
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 FT 259. .379
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 FT 274. .279
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 FT 416. .424
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 FT Domain
 FT 428. .448
 FT /note= "Transmembrane domain"
 PN WO200216429-A2.
 XX
 XX PD 28-FEB-2002.
 XX PR 22-JUN-2001; 2001WO-US020118.
 XX PR 24-AUG-2000; 2000WO-US023328.
 PR 26-SEP-2000; 2000US-0235451P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V;
 PI Wood WI, Wu TD, Zhang Z;
 XX DR WPI; 2002-280917/32.
 DR N-PSDB; ABK11093.
 XX
 PT Novel isolated tumor-associated antigenic target polypeptides which are
 PT useful as targets for cancer therapy and diagnosis in mammals.
 XX
 PS Claim 12; Fig 10; 121pp; English.
 XX
 CC The invention relates to an isolated tumour-associated antigenic target
 CC polypeptide (TAT) (I), specifically TAT134-TAT138 polypeptides, and the
 CC polyimides (II) encoding them. (II) is useful for diagnosing the
 presence of a tumour in a mammal, where the level of expression of (II)
 CC is indicative on the presence of tumour in the mammal from which the test
 sample was obtained. Antibody to (I) is useful for killing a cancer cell
 (e.g. breast cancer cell, a colorectal cancer cell, a lung cancer cell,
 CC an ovarian cancer cell, a central nervous system (CNS) cancer cell, a
 liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a
 CC melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides
 CC hybridising to (II) are useful as diagnostic probes, antisense
 CC oligonucleotide probes or for encoding fragments of full length TAT
 CC polypeptide. (II) is also useful in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA probes, for constructing
 CC hybridisation probes for mapping the gene encoding TAT and for genetic
 CC analysis of individuals with genetic disorders. (II) is also useful for
 CC generating either transgenic animals or knockout animals, and in gene
 CC therapy. The TAT polypeptides and nucleic acids may also be used for
 CC tissue typing and the TAT polypeptides are useful for screening compounds
 CC that mimic the TAT polypeptide (agonist) or prevent the effect of TAT
 CC polypeptide (antagonist). The antibody is useful for staging TAT

CC polypeptide-expressing cancers, purifying or immunoprecipitating TAT
 CC polypeptide from cells, for detection and quantitation of TAT polypeptide
 CC in vitro, e.g., in an enzyme linked immunosorbent assay (ELISA) or
 CC Western blot. The antibodies are also useful for treating a TAT-
 CC expressing cancer or alleviating one or more symptoms of cancer in a
 CC mammal. The present sequence represents the amino acid sequence of TAT138
 XX SQ Sequence 454 AA:

Query	Match	Score	DB	Length
Best	Local	100.0%	5;	454;
Matches	Conservative	100.0%	Pred.	No. 5e-245;
		0;	Mismatches	0;
		0;	Indels	0;
		0;	Gaps	0;

Qy 1 MESISMGSPPSLSSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLRCGYHVG
 Db 1 MESISMGSPPSLSSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLRCGYHVG 60
 Qy 61 RNPKEASEEFFPHVVDVTHEDALTKTNTIFAVHLRLLHGKLLIDVSNNM 120
 Db 61 RNPKEASEEFFPHVVDVTHEDALTKTNTIFAVHLRLLHGKLLIDVSNNM 120
 Qy 121 RINQYQPESSNAEYLASLFPDSLIVKGFTNSAWALQGPDKASROVYICSNNIQARQQVIE 180
 Db 121 RINQYQPESSNAEYLASLFPDSLIVKGFTNSAWALQGPDKASROVYICSNNIQARQQVIE 180
 Qy 181 LARQLNFIPIIDIGSLSISSAREIENLPLRLFTLWRGPVVVAISLATEFFFLYSFVRDVTHPYA 240
 Db 181 LARQLNFIPIIDIGSLSISSAREIENLPLRLFTLWRGPVVVAISLATEFFFLYSFVRDVTHPYA 240
 Qy 241 RNQSDFYKIPIEVNKTLPIVAITLISVLYLAGLLAAQOLYYGKRYRFPPLWTLQ 300
 Db 241 RNQSDFYKIPIEVNKTLPIVAITLISVLYLAGLLAAQOLYYGKRYRFPPLWTLQ 300
 Qy 301 CRKQLGLSFFPEAMVHVAISLCLPMERSERYLFLNMAQOQHANIENSWNNEEEVWRIEMY 360
 Db 301 CRKQLGLSFFPEAMVHVAISLCLPMRSERYLFLNMAQOQHANIENSWNNEEVWRIEMY 360
 Qy 361 ISFGIMSLGLLILLLAVTSIPSVSNALNREFSFIOSTIGYALLISTFHVLTYGWKRAFE 420
 Db 361 ISFGIMSLGLLILLLAVTSIPSVSNALNREFSFIOSTIGYALLISTFHVLTYGWKRAFE 420
 Qy 421 EEXYRFYTTPNFTVALVLPSPIVILDILQLCRYPD 454
 Db 421 EEXYRFYTTPNFTVALVLPSPIVILDILQLCRYPD 454
 WO200226822-A2.

RESULT 5
 ID AAU80190
 ID AAU80190 standard; protein; 454 AA.
 AC AAU80190;
 XX DT 15-JUL-2002 (first entry)
 XX DE Human PUMPCn protein, PRO23203.
 XX KW Human; protein upregulated in metastatic prostate cancer; immunogen; PUMPCn; PRO23203; prostate cancer; cytostatic; gene therapy; transgenic; androgen independent prostate cancer; DNA microarray.
 XX OS Homo sapiens.
 XX PN WO200226822-A2.
 XX PD 04-APR-2002.
 XX PR 26-SEP-2001; 2001WO-US030290.
 XX PR 26-SEP-2000; 2000US-0235451P.
 XX PA (GETH) GENENTECH INC.
 XX PI Devaux B, Eberhard D, Goddard A, Godowski PJ, Grimaldi JC;

PI Hillan KJ, Watanabe CK, Wood WI, Yansura DG, Zhang Z;
 XX
 DR WPI; 2002-383270/41.
 N-PSDB; ABK50391.

PT New polypeptide termed protein upregulated in metastatic prostate cancer and encoding polynucleotides, useful for identifying polypeptide antagonists for treating prostate cancer.

XX PS Claim 23; Fig 2; 137pp; English.

CC The invention relates to an isolated human protein upregulated in metastatic prostate cancer (PUMPCn) PRO23203 polypeptide, a sequence 80% identical to PRO23203 and the sequence as encoded by cDNA insert of the vector deposited as ATCC Deposit No. PTA-2513 (DNA185171-2994) on 26/9/2000. Also included are the polynucleotide encoding the protein (or a DNA sequence 80% identical to the polynucleotide and one that hybridises to complement of the polynucleotide), a vector comprising the polynucleotide, a polynucleotide deposited with ATCC under accession number PTA-2513 (DNA185171-2994), a host cell comprising the vector, preparation of PRO23203, a chimeric molecule comprising PRO23203 fused to a heterologous amino acid sequence, an anti-PRO23203 antibody, an agonist/antagonist of PRO23203, and diagnosing the presence of prostate cancer in a mammal by: (a) contacting a microarray diagnostic with a DNA185171-2994 probe, detecting and quantifying hybridisation of DNA185171-2994 probe in prostate cancer tissue compared with normal tissue and determining if DNA185171-2994 is overexpressed; or (b) contacting a tissue of the mammal with an anti-PRO23203 antibody and detecting the binding of the antibody to a component of the tissue, where binding is indicative of the presence of prostate cancer in the mammal. The antibody is useful for treating prostate cancer in mammal which is androgen independent prostate cancer, that has metastasised to another portion of the body, where the antibody is not conjugated with a cytotoxic agent and the method further comprises administering a chemotherapeutic agent to the mammal and for diagnosing the presence of prostate cancer in an mammal. The PRO23203 polynucleotide is useful for generating either transgenic animals or knock out animals which in turn are useful in the development and screening of therapeutically useful reagents or for use in gene therapy and for chromosome identification. PRO23203 and polynucleotide may also be used for tissue typing and PRO23203 may also be employed as a therapeutic agents and for screening compounds to identify those that mimic the PRO23203 polypeptides (agonists) or prevent the effect of the PRO23203 polypeptide (antagonists). PRO23203 is further useful for the affinity purification of PRO23203 from recombinant cell culture or natural sources. The present sequence represents PRO23203

XX SQ Sequence 454 AA;

Query Match 100.0%; Score 2351; DB 5; Length 454;
 Best Local Similarity 100.0%; Pred. No. 5e-245; Mismatches 0; Indels 0; Gaps 0;
 Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGMGSPKSLSETCLPNGINGIKDARKTVGVIGSDFAKSLTIRLIRCGYHVG 60
 1 MESISMGMGSPKSLSETCLPNGINGIKDARKTVGVIGSDFAKSLTIRLIRCGYHVG 60

Db 61 RNPKEASEFFPHVVDVTMHEDALTAKNIFVIAHREHYTSIWLDRHLVKGKILDVSNNM 120
 61 RNPKEASEFFPHVVDVTMHEDALTAKNIFVIAHREHYTSIWLDRHLVKGKILDVSNNM 120

QY 121 RINQYPESNAEYLASLPDSLIVKGPNVSAWALQLGPDKASRQVICSNNIQARQVIE 180
 121 RINQYPESNAEYLASLPDSLIVKGPNVSAWALQLGPDKASRQVICSNNIQARQVIE 180

Db 181 LARQINFIPIDGLSLSAREIENPLRFLTWRGPVVAISLATEFLISFVRDVHRYA 240
 181 LARQINFIPIDGLSLSAREIENPLRFLTWRGPVVAISLATEFLISFVRDVHRYA 240

QY 241 RNQOSDFYKIPIEIWKTLPIAVITLISLYLAGLAAAYQLYIGTKYRFPWPLETWQ 300
 241 RNQOSDFYKIPIEIWKTLPIAVITLISLYLAGLAAAYQLYIGTKYRFPWPLETWQ 300

Oy 301 CRKQIGLILSPPFAMVHVAYSICLCPMRRSERYLFINMAYQOQHANTENSWNTEEVRIEMY 360
 Db 301 CRKQIGLILSPPFAMVHVAYSICLCPMRRSERYLFINMAYQOQHANTENSWNTEEVRIEMY 360

Oy 361 ISFGIMSIGLSSLLAVTSIPSVSNALNREFSFTOSTLGYVALLISTEHVLIYGWRAFE 420
 Db 361 ISFGIMSIGLSSLLAVTSIPSVSNALNREFSFTOSTLGYVALLISTFHVLIVGWWRAFE 420

Oy 421 EEXYRFYTPPNFVIALVLPSTVILDLQLCRYPD 454
 Db 421 EBYYRFYTPPNFVIALVLPSTVILDLQLCRYPD 454

Qy RESULT 6
 ID ABU08893 standard; protein; 454 AA.
 XX ABU08893;
 AC
 XX DT 09-OCT-2003 (first entry)
 DE Tumour-associated antigenic target 138 (TAT138).
 KW Human; tumour-associated antigenic target polypeptide; TAT; tumour; gene therapy; cytostatic; tissue typing; prostate tumour; cancer.
 OS Homo sapiens.
 XX PN US2003060612-A1.
 XX PD 27-MAR-2003.
 XX PP 22-JUN-2001; 2001US-00888257.
 XX PR 28-OCT-1997; 97US-0063540P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 26-SEP-2000; 2000US-0235451P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.

XX PA (GETH) GENENTECH INC.

XX PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith V;
 PI Wood WI, Wu TD, Zhang Z;
 DR WPI; 2003-576355/54.
 N-PSDB; ACD25893.

XX PT New nucleic acid, useful for the manufacture of a medicament for
 PT diagnosing or treating tumor in a mammal.
 XX PS Claim 12; Fig 10; 71pp; English.

XX The invention discloses human nucleic acids encoding tumour-associated antigenic target (TAT) polypeptides, with or without their associated signal peptide. Also disclosed is an antibody that specifically binds to the TAT polypeptides, a method for detecting the presence of a tumour in a mammal and a method for killing a cancer cell expressing the TAT polypeptide. The nucleotide sequences are useful in preparing TAT polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The TAT polypeptides are useful as therapeutic agents and for detecting the presence, prevention and/or treatment of a tumour, such as colon, breast or prostate tumour. The TAT polypeptides and nucleic acids may also be used diagnostically for tissue

RESULT 8

AAE28951
ID AAE28951 standard; protein; 490 AA.
XX
AC AAE28951;
XX DT 27-JAN-2003 (first entry)
XX DE Human STEAPRP protein.
KW Human; STEAPRP; proliferative disorder; prostate hyperplasia; cancer;
six-transmembrane epithelial antigen of the prostate related protein;
gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN WO200272596-A1.
XX PD 19-SEP-2002.
XX PF 07-MAR-2002; 2002WO-US007053.
XX PR 09-MAR-2001; 2001US-00802520.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PT Lal PG, Faris M, Chen H, Ison CH;
XX DR WPI; 2002-723311/78.
DR N-PSDB; AAD46429.
XX PT New six-transmembrane epithelial antigen of the prostate-related protein
and nucleic acids; useful for diagnosing and treating prostate cell
proliferative disorders, particularly prostate hyperplasia and prostate
cancer.
PT XX PS Claim 13; Page 54-55; 62pp; English.
CC The invention relates to six-transmembrane epithelial antigen of the
prostate related protein (STEAPRP) and its corresponding nucleic acid.
CC STEAPRP DNA is used to diagnose and to treat prostate cell proliferative
disorders, particularly prostate hyperplasia and prostate cancer, and for
screening a library of molecules of compounds for specific binding
affinity. It is also used in gene therapy. STEAPRP is used to screen a
subject sample for antibodies, which specifically binds the protein, and
to prepare and purify a protein. The present sequence is human STEAPRP
protein.
CC XX SQ Sequence 490 AA;

Query Match 97.6%; Score 2294; DB 5; Length 490;
Best Local Similarity 100.0%; Pred. No. 8.4e-239; Mismatches 0; Indels 0; Gaps 0;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
1 MESISMGMSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVG 60
Qy 61 RNPKEASEFPHVVDVTHEDALTKTNIIFVAIHRHYTLSWDLRHLLVGKLLIDVSNNM 120
61 RNPKEASEFPHVVDVTHEDALTKTNIIFVAIHRHYTLSWDLRHLLVGKLLIDVSNNM 120
Db 121 RINOQPESNAYELASLFPDSLIVKGFNVSAWALQGPKDASRQWYICSNNIQARQVIE 180
121 RINOQPESNAYELASLFPDSLIVKGFNVSAWALQGPKDASRQWYICSNNIQARQVIE 180
Qy 181 LARQLNFIPIIDLGSLSAREIENPLRLFTIWRGPVVAISLATFFFLYSFVRDVHYP 240
181 LARQLNFIPIIDLGSLSAREIENPLRLFTIWRGPVVAISLATFFFLYSFVRDVHYP 240
Db 241 RNQQSDFYKIPIEIVNKTLPIVAILLISLWVLAGLLAAVQLYYGTYYRFPMLETWLO 300
241 RNQQSDFYKIPIEIVNKTLPIVAILLISLWVLAGLLAAVQLYYGTYYRFPMLETWLO 300

RESULT 9

ABU63312
ID ABU63312 standard; protein; 490 AA.
XX AC ABU63312;
XX DT 18-SEP-2003 (first entry)
XX DE Human transmembrane protein TMPL.
XX KW Human; prostate tumour; lung tumour; TMPL; cancer.
XX OS Homo sapiens.
XX PN US2003064397-A1.
XX PD 03-APR-2003.
XX PF 24-JUL-2002; 2002US-00205267.
XX PR 22-MAY-1998; 98US-00083521.
PR 16-SEP-1999; 99US-00397558.
PR 09-MAR-2001; 2001US-00802520.
PR 26-SEP-2001; 2001US-00963896.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Spancake KM, Rickert PK, Lal PG, Ison CH;
XX DR WPI; 2003-540783/51.
DR N-PSDB; ACD27642.
XX PT New transmembrane protein differentially expressed in prostate and lung
tumors, useful for diagnosing, staging, treating or monitoring
progression or treatment of cancer, preferably lung or prostate cancer.
XX PS Claim 1; Fig 1; 49pp; English.

Qy CC The invention relates to a purified human protein comprising a
polypeptide having a fully defined transmembrane protein differentially
expressed in prostate and lung tumor (TMPL) sequence. The protein is
useful for detecting expression of the protein in a sample, where the
sample is lung or prostate tissue sample and the protein is
differentially expressed when compared with a standard and is diagnostic
of a lung or prostate cancer. The protein is useful to identify an
antibody that specifically binds the protein. The protein is useful for
screening several molecules and compounds to identify at least one
ligand. The protein is also useful for preparing and purifying a
polyclonal antibody and for preparing a monoclonal antibody using
standard animal immunisation/hybridoma methods. A TMPL specific antibody
is useful to detect expression of the protein in a lung or prostate
tissue sample and the method is useful as a diagnostic for lung or
prostate cancer. A TMPL specific antibody is also useful for
immunopurifying a protein, for treating a prostate cancer and for
delivering a therapeutic agent to a cancer, preferably prostate cancer.
The protein is useful for diagnosing, staging, treating or monitoring
progression or treatment of cancer, preferably lung or prostate cancer.
The present sequence represents the amino acid sequence of the human

Db 241 RNQQSDFYKIPIEIVNKTLPIVAILLISLWVLAGLLAAVQLYYGTYYRFPMLETWLO 300
Qy 301 CRKQOLGLSFFPMVHVAYSILCPLMRSERYLPLNMAYQVHANIENSWNEEVRIEMY 360
Db 301 CRKQOLGLSFFPMVHVAYSILCPLMRSERYLPLNMAYQVHANIENSWNEEVRIEMY 360
Qy 361 ISFGIMSLGILSLAVTSIPSVSNALNWREFSPQSTLGIVALLISTFFVLIYGWRAFE 420
Db 361 ISFGIMSLGILSLAVTSIPSVSNALNWREFSPQSTLGIVALLISTFFVLIYGWRAFE 420

Qy 421 EYVRYFYTTPNVLAVLVLPSIVL 444
Db 421 EYVRYFYTTPNVLAVLVLPSIVL 444

CC	transmembrane protein differentially expressed in prostate and lung
CC	tumour TMPL
XX	Sequence 490 AA;
XX	Query Match 97.6%; Score 2294; DB 7; Length 490;
XX	Best Local Similarity 100.0%; Pred. No. 8.4e-239;
XX	Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	Db 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVVIGSGDFAKSLTIRLIRCGYHNVIGS 60
QY	61 RNPKFASEFFPHWVDVTHEDALTNTNIFVAIHERHTSLWDLRHLLVGKILLDVSNM 120
Db	121 RINOYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIOARQVIE 180
QY	121 RINOYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIOARQVIE 180
Db	181 LARQINFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
QY	181 LARQINFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
Db	181 LARQINFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
QY	241 RNOQSDFYKIPIEVNKTLPVIAITLLSVLAGLLAAAYQLYGTYRKRRFPWPLETWQ 300
Db	241 RNOQSDFYKIPIEVNKTLPVIAITLLSVLAGLLAAAYQLYGTYRKRRFPWPLETWQ 300
QY	301 CRKQIGLISFFRAMHVAYSICLPMRRSERYLFLNMAQQVHANTENSNEEWRIEMY 360
Db	301 CRKQIGLISFFRAMHVAYSICLPMRRSERYLFLNMAQQVHANTENSNEEWRIEMY 360
QY	361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIOSTLGVALLISTFHVLIGWKRAFE 420
Db	361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIOSTLGVALLISTFHVLIGWKRAFE 420
QY	421 EYYRFYTPPNFVLLVLP SIVIL 444
Db	421 EYYRFYTPPNFVLLVLP SIVIL 444
XX	RESULT 10
AAU10187	ID AAU10187 standard; protein; 490 AA.
XX	AC AAU10187;
XX	DT 16-JAN-2002 (first entry)
DE	Human Six-Transmembrane Protein of Prostate 1, STM1.
XX	Human; Six-Transmembrane Protein of Prostate 1; STM; 1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer and lung cancer.
XX	Homo sapiens.
XX	Key Location/Qualifiers
FT	Domain 209..230 /label= Transmembrane_domain_1
FT	Domain 255..273 /label= Transmembrane_domain_2
FT	Domain 304..325 /label= Transmembrane_domain_3
FT	Domain 360..380 /label= Transmembrane_domain_4
FT	Domain 393..415 /label= Transmembrane_domain_5
FT	Domain 432..452 /label= Transmembrane_domain_6
XX	Query Match 97.4%; Score 2290; DB 4; Length 490;
XX	Best Local Similarity 99.8%; Pred. No. 2.3e-238;
XX	Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX	Db 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVVIGSGDFAKSLTIRLIRCGYHNVIGS 60
QY	61 RNPKFASEFFPHWVDVTHEDALTNTNIFVAIHERHTSLWDLRHLLVGKILLDVSNM 120
Db	121 RINOYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIOARQVIE 180
QY	121 RINOYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIOARQVIE 180
Db	181 LARQINFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
QY	181 LARQINFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
Db	241 RNOQSDFYKIPIEVNKTLPVIAITLLSVLAGLLAAAYQLYGTYRKRRFPWPLETWQ 300
QY	241 RNOQSDFYKIPIEVNKTLPVIAITLLSVLAGLLAAAYQLYGTYRKRRFPWPLETWQ 300
Db	301 CRKQIGLISFFRAMHVAYSICLPMRRSERYLFLNMAQQVHANTENSNEEWRIEMY 360
QY	361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIOSTLGVALLISTFHVLIGWKRAFE 420
Db	361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIOSTLGVALLISTFHVLIGWKRAFE 420
QY	421 EYYRFYTPPNFVLLVLP SIVIL 444

Db 421 |EYVRFITPPNFTLALVLP SIVI| 444 Qy 121 RINQYEPESNAEYLASLFPSDLITVKGFNVSAWAIQIGPKDASRQVYTCNNIOARQQVTE 180
 Db AAU10189 standard; protein; 419 AA. Qy 121 RINQYEPESNAEYLASLFPSDLITVKGFNVSAWAIQIGPKDASRQVYTCNNIOARQQVTE 180
 ID AAU10189 XX
 AC AAU10189; XX
 DT 16-JAN-2002 (first entry) XX
 DE Human ORF3 of Six-Transmembrane Protein of Prostate 1. XX
 KW Human; Six-Transmembrane Protein of Prostate 1; STM; 1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; liver cancer; lung cancer; cytostatic; ORF3. XX
 OS Homo sapiens. XX
 PN WO200172962-A2. PN
 PD 04-OCT-2001. PD
 XX ABG12306 standard; protein; 576 AA. XX
 PF 23-MAR-2001; 2001WO-US009410. AC ABG12306; XX
 PR 24-MAR-2000; 2000US-0191929P. DT 18-FEB-2002 (first entry) XX
 PA (SAAT/) SAATCIOGLU F. DE Novel human diagnostic protein #12297. XX
 PI Saatcioglu F; XX
 DR N-PSDB; AAS15813. OS Homo sapiens. XX
 PT New polynucleotide for the diagnosis, prevention and treatment for DR
 PT prostate and testis disorders, particularly prostate cancer, comprises OS
 PT prostate-specific or testis-specific nucleic acids. PN
 BS Claim 1; Fig 4K; 114pp; English. XX
 CC The invention relates to substantially pure prostate-specific or testis-specific polypeptides and the nucleic acids encoding them. Also included CC
 CC are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for detecting the nucleic acids, antisense molecules for the nucleic acids CC
 CC and methods of isolating modulators of the proteins. Compounds that module the prostate specific or testis specific polypeptide are useful CC
 CC to diagnose, prevent or treat disorders of the testis or prostate particularly prostate cancer, benign prostatic hyperplasia, acute CC
 CC prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the CC
 CC modulators may be used include lymphoma, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. CC
 CC The present sequence is prostate specific protein, Six-Transmembrane Protein of Prostate 1, STM;1, ORF3. XX
 SQ Sequence 419 AA;
 Query Match 86.6%; Score 2036; DB 4; Length 419;
 Best Local Similarity 99.7%; Pred. No. 5.5e-211;
 Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MESISMGGSPKSLSSETCLPNGINGIKDARKTVGVIGSGDFAKSLITIRCGHVG 60 Qy 1 MESISMGGSPKSLSSETCLPNGINGIKDARKTVGVIGSGDFAKSLITIRCGHVG 60
 Db 1 MESISMGGSPKSLSSETCLPNGINGIKDARKTVGVIGSGDFAKSLITIRCGHVG 60 Db 1 MESISMGGSPKSLSSETCLPNGINGIKDARKTVGVIGSGDFAKSLITIRCGHVG 60
 Qy 61 RNPKFASEFFPHWVDVTHEDALKTNTIFVAIHERHYSLSLWDLRHLIWKTKLIDVSNNM 120 Qy 61 RNPKFASEFFPHWVDVTHEDALKTNTIFVAIHERHYSLSLWDLRHLIWKTKLIDVSNNM 120
 Db 61 RNPKFASEFFPHWVDVTHEDALKTNTIFVAIHERHYSLSLWDLRHLIWKTKLIDVSNNM 120 Db 61 RNPKFASEFFPHWVDVTHEDALKTNTIFVAIHERHYSLSLWDLRHLIWKTKLIDVSNNM 120

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC [ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences)
 XX SQ Sequence 576 AA;

Query Match 83.9%; Score 1972.5; DB 4; Length 576;
 Best Local Similarity 87.4%; Pred. No. 6.7e-204; Indels 55; Gaps 1;
 Matches 390; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVG 60
 QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVG 60
 QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHCHEHTSLSWDLRHLVGKILIDVSNNM 120
 QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHCHEHTSLSWDLRHLVGKILIDVSNNM 120
 Db 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPDKASRQVTCNSNIIQARQVIE 180
 Db 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPDKASRQVTCNSNIIQARQVIE 180
 Db 181 LARQINFIPIDGLSLSAREIENLPLRLFTLWRGPVVAISLATPFLYSFVRDVHPIYA 240
 Db 181 LARQINFIPIDGLSLSAREIENLPLRLFTLWRGPVVAISLATPFLYSFVRDVHPIYA 240
 Db 180 LARQINFIPIDGLSLSAREIENLPLRLFTLWRGPVVAISLATPFLYSFVRDVHPIYA 240
 Db 241 RNQQSDFYKIPIEVNKTLPIVAITLISLVLAGLLAAVQLYYGTKRREPPWLETWQ 300
 Db 241 RNQQSDFYKIPIEVNKTLPIVAITLISLVLAGLLAAVQLYYGTKRREPPWLETWQ 300
 QY 301 CRKQIGLISFFAMVHVAYSLCLPMRRSERYLFINMAYQOVHANTENSNEEEVWRIMEY 360
 QY 301 CRKQIGLISFFAMVHVAYSLCLPMRRSERYLFINMAYQOVHANTENSNEEEVWRIMEY 360
 Db 301 CRKQIGLISFFAMVHVAYSLCLPMRRSERYLFINMAYQOVHANTENSNEEEVWRIMEY 360
 QY 361 ISFGIMSLGLLAVTSIPSVSNALNWREFSFIQSTLGIVALLISTFHVLIGWKRAFE 420
 QY 361 ISFGIMSLGLLAVTSIPSVSNALNWREFSFIQSTLGIVALLISTFHVLIGWKRAFE 420
 Db 340 - - - - - QSTLGIVALLISTFHVLIGWKRAFE 365
 QY 421 EYYRFYTPPNFVLALVLPSTIVLDL 446
 Db 366 EYYRFYTPPNFVLALVLPSTIVLDL 391

PI Drmanac RT, Liu C, Tang YT,
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS64300.

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX PS Claim 20; SEQ ID NO 30472; 103PP; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
[ftp.wipo.int/pub/published_pct_sequences](ftp://wipo.int/pub/published_pct_sequences)

XX SQ Sequence 1273 AA;

Query Match 83.9%; Score 1972.5; DB 4; Length 1273;
 Best Local Similarity 87.4%; Pred. No. 2.3e-203; Indels 55; Gaps 1;
 Matches 390; Conservative 0; Mismatches 1; Indels 55; Gaps 1;

QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVG 60
 QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVG 60
 Db 73 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVG 132
 QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHCHEHTSLSWDLRHLVGKILIDVSNNM 120
 QY 61 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHCHEHTSLSWDLRHLVGKILIDVSNNM 120
 Db 133 RNPKFASEFFPHVVDVTHEDALTKTNIIFVAIHCHEHTSLSWDLRHLVGKILIDVSNNM 192
 QY 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPDKASRQVTCNSNIIQARQVIE 180
 QY 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPDKASRQVTCNSNIIQARQVIE 180
 Db 193 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPDKASRQVTCNSNIIQARQVIE 252
 AC ABG00113;
 AC ABG00113;
 XX DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #104.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX PD 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-0054217.
 PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.

RESULT 14

ID AAE02841

AAE02841 standard; protein; 450 AA.

XX

AC AAE02841;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human STEAP-2 protein, alternative version.

XX

KW Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian; pancreatic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 335. .336 /note= "Encoded by GACTGAGCT"

FT Misc-difference 375. .376 /note= "Encoded by AGATGAAGT"

FT Misc-difference 415. .416 /note= "Encoded by GAGTAGGC"

FT Misc-difference 445. .446 /note= "Encoded by ACATGAACT"

FT Misc-difference 448. .449 /note= "Encoded by ATTAAATTC"

XX

PN WO200140276-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US033040.

XX

PR 06-DEC-1999; 99US-00455486.

XX

PA (URRG-) UROGENESYS INC.

XX

PI Afar DEH, Hubert RS, Raitano AB, Saffran DC, Mitchell SC;

PI Paris M, Jakobovits A;

XX WPI; 2001-367804/38.

DR N-PSDB; AAD07072.

XX

PT New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating cancer.

PT

XX

PS Claim 1; Page 175-176; 187pp; English.

XX

CC The present sequence is an alternative version of human six transmembrane epithelial antigen of the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (e.g. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly. Note: This sequence is stated to be the same as that being shown as SEQ ID NO:8 (AAE02781) in figure 9A-9C of the specification. However the present sequence lacks several amino acids at its N-terminal end and has additional amino acids at its C-terminal end when compared with the sequence shown in figure 9A-9C

XX

SQ Sequence 450 AA;

Query Match 73.9%; Score 1738; DB 4; Length 450; Best Local Similarity 100.0%; Pred. No. 1.1e-178; Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 NMRINQYPESNAEYLASLFPDSLIVKGFNVSAAWALQLGPKDASRQVICSNNIQARQQV 178

Db 1 NMRINQYPESNAEYLASLFPDSLIVKGFNVSAAWALQLGPKDASRQVICSNNIQARQQV 60

QY 179 IELARQINFIPIDGLSISAREIENPLRLIFTLWRGPVVVAISLATFFLYSFVRDVTHP 238

Db 61 IELARQINFIPIDGLSISAREIENPLRLIFTLWRGPVVVAISLATFFLYSFVRDVTHP 120

QY 239 YARNQOSDFYKIPIEVNKTLPIVAITLSSLVYLAGLLAAQOLYYGTYRKRRFPWLETW 298

Db 121 YARNQOSDFYKIPIEVNKTLPIVAITLSSLVYLAGLLAAQOLYYGTYRKRRFPWLETW 180

QY 299 LQCRQOLGLISFFAMVHAYSLCLPMRRSERYLFINMAYQVHANIENSNEEWRIE 358

Db 181 LQCRQOLGLISFFAMVHAYSLCLPMRRSERYLFINMAYQVHANIENSNEEWRIE 240

QY 359 MYISFGIMSLGLLSLAVTSIPSVSNALNWRFSFIQSTLGVALLISTFHVLIVYWKRA 418

Db 241 MYISFGIMSLGLLSLAVTSIPSVSNALNWRFSFIQSTLGVALLISTFHVLIVYWKRA 300

QY 419 FEEYYRFYTPPNFVIALVLPSSIVIDLQLCRYD 454

Db 301 FEEYYRFYTPPNFVIALVLPSSIVIDLQLCRYD 336

RESULT 15

ID ABP62883

XX ABP62883 standard; protein; 1082 AA.

XX

AC ABP62883;

XX

DT 14-OCT-2002 (first entry)

XX

DE Human polypeptide SEQ ID NO 320.

XX

KW Human; vulnery; dermatological; neuroprotective; nootropic; cancer; anti-parkinsonian; immunostimulant; cytostatic; immunosuppressive; anti-diabetic; anti-allergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.

XX

OS Homo sapiens.

XX

PN WO200218424-A2.

XX

PD 07-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-US027093.

XX

PR 01-SEP-2000; 2000US-00654935.

XX

PA (HYSE-) HYSEQ INC.

XX

Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;

PI Zhao QA, Wang D, Liu C, Dumanac RT, Wehrman T;

XX

WPI; 2002-583321/62.

DR N-PSDB; ABQ93362.

XX

PT New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

XX

PS Claim 20; SEQ ID NO 320; 284pp + Sequence Listing; English.

XX

CC The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising

CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 1082 AA;

Query	Match	Score	DB	Length
QY	Best Local Similarity 83.2%; Pred. No. 1.1e-137; Matches 272; Conservative 0; Mismatches 0; Indels 55; Gaps 1;	58.0%	5	1082;
Db	1 MRINQYPESSNAEYLAISLFPDSLIVKGPNVVSAAWALQOLGGPKDASRQVYICSNNIQARQVI 179			
QY	120 MRINQYPESSNAEYLAISLFPDSLIVKGPNVVSAAWALQOLGGPKDASRQVYICSNNIQARQVI 179			
Db	121 ELARQLINEPIDLGSSISSAREIEENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVTHPY 239			
QY	61 ELARQLINEPIDLGSSISSAREIEENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVTHPY 239			
Db	180 ELARQLINEPIDLGSSISSAREIEENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVTHPY 239			
QY	240 ARNQOSDFYKIPIBIWKTLPIAVITLISLYLAGLLAAAYQLYGTYRKYRFPFWLETWL 299			
Db	241 ARNQOSDFYKIPIBIWKTLPIAVITLISLYLAGLLAAAYQLYGTYRKYRFPFWLETWL 299			
QY	121 ARNQOSDFYKIPIBIWKTLPIAVITLISLYLAGLLAAAYQLYGTYRKYRFPFWLETWL 299			
Db	300 QCRKQGLLISFFPAMHVAYSLCPMRRSERYXLFLNMAQQVHANTENSWEEVWRIEM 359			
QY	181 QCRKQGLLISFFPAMHVAYSLCPMRRSERYXLFLNMAQQVHANTENSWEEVWRIEM 359			
Db	182 QCRKQGLLISFFPAMHVAYSLCPMRRSERYXLFLNMAQQVHANTENSWEEVWRIEM 359			
QY	220 QCRKQGLLISFFPAMHVAYSLCPMRRSERYXLFLNMAQQVHANTENSWEEVWRIEM 359			
Db	360 YISPGIMSLGLLISLLAVTSIPSNSNALWREFSFIQSTLGYVALLISTFHVLILYGWKR 419			
QY	221 - - - - - QSTLGYVALLISTFHVLILYGWKR 419			
Db	420 EEEYYRFYTPPNFVLALVLPSIVILDL 446			
QY	246 EEEYYRFYTPPNFVLALVLPSIVILDL 272			

Search completed: March 1, 2004, 23:33:05
 Job time : 102 secs

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OM protein - protein search, using sw model

Run on:

March 1, 2004, 23:31:21 ; Search time 45 Seconds

(without alignments)
970.466 Million cell updates/sec

Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESISMGSPLSILETCLPN.....ALVLPSSIVLDLQLCRYPD 454

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	160	6.8	198	2	D95285	conserved hypothetical protein Sma0349 [imported] - <i>Sinorhizobium meliloti</i> (strain 1021 C;Species: <i>Sinorhizobium meliloti</i> C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: D95285 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Barloy-Hubler, F.; Bowe, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire <i>Sinorhizobium meliloti</i> genome A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: D95285 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-198 <KUR> A;Cross-references: GB:AE006469; PIDN:AAK64846.1; PID:914523260; GSPDB:GN00165 A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Delpal, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauze, H.; Lebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont <i>Sinorhizobium meliloti</i> . A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: C;Gene: Sma0349 A;Genome: Plasmid
2	159.5	6.8	211	2	AC2560	conserved hypothetical prote
3	156.5	6.7	239	2	T50571	probable oxidoredu
4	147	6.3	213	2	H69400	conserved hypothet
5	142	6.0	212	2	D69361	conserved hypothet
6	142	6.0	224	2	T10120	F420-dependent NAD
7	133	5.7	223	2	D64487	hypothetical prote
8	121	5.1	191	2	F86826	hypothetical prote
9	120.5	5.1	232	2	A69131	conserved hypothet
10	119.5	5.1	216	2	T00121	hypothetical prote
11	116.5	5.0	242	2	G82642	conserved hypothet
12	116	4.9	198	2	AB3182	conserved hypothet
13	111.5	4.7	695	1	JN0898	follitropin recept
14	111.5	4.7	1228	2	S59681	probable membrane
15	110.5	4.7	222	2	B84410	hypothetical prote
16	110.5	4.7	694	2	JC4301	follitropin recept
17	109	4.6	320	2	T28379	ORF MSV218 hypoth
18	109	4.6	712	2	S50969	probable membrane
19	109	4.6	1184	2	H71436	hypothetical prote
20	109	4.6	1301	2	D85188	disease resistance
21	107.5	4.6	629	2	S60385	probable membrane
22	107.5	4.6	695	1	QRHUFFT	follitropin recept
23	105	4.5	442	2	B64582	sodium- and chlori
24	105	4.5	604	2	T31042	hypothetical prote
25	104	4.4	396	1	C64907	chloramphenicol re
26	104	4.4	396	2	G90895	hypothetical prote
27	104	4.4	396	2	H85721	probable resistanc
28	103	4.4	465	2	S69915	sodium-phosphate t
29	102.5	4.4	314	2	AB2972	hypothetical prote

ALIGNMENTS

RESULT 1

D95285

conserved hypothetical protein Sma0349 [imported] - *Sinorhizobium meliloti* (strain 1021

C;Species: *Sinorhizobium meliloti* C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: D95285 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Barloy-Hubler, F.; Bowe, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* genome A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: D95285 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-198 <KUR> A;Cross-references: GB:AE006469; PIDN:AAK64846.1; PID:914523260; GSPDB:GN00165 A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Delpal, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauze, H.; Lebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*. A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: C;Gene: Sma0349 A;Genome: Plasmid

probable peptide A
probable mRNA stab
bicyclomycin resis
hypothetical prote
hypothetical prote
NADH2 dehydrogenas
O-antigen transpor
hypothetical glucan sy
hypothetical prote
hypothetical prote
endonuclease Scel
ABC transporter AT
NADH2 dehydrogenas

probable peptide A
bicyclomycin resis
hypothetical prote
hypothetical prote
hypothetical prote
NADH2 dehydrogenas
probable glucan sy
hypothetical prote
endonuclease Scel
ABC transporter AT
NADH2 dehydrogenas

RESULT 2

139 DSLINKGFNVSSAWALQLGPK-DASRQVYICSNQIQRQQVIELARQINFIPIIDLGSLS 138

62 VVILAV--PYDSDIADIVTVQSDWGGQIVVDASNAIDFPFPKPRDLGGRLISTEVSELVP 118

119 GAKVVKAFNTLPAVLAADPDKGTCGSRVLFSLSGNHSANROVAELLISSIGFAPVDLGLTA 178

197 SAREIENLPLRLFTLWRGPVVVAISL 222

179 ASGPIQOF-----GRPLVALNL 195

H69400

Query Match 6.0%; Score 142; DB 2; Length 212;
 Best Local Similarity 25.4%; Pred. No. 0.0006; PMID:8688087
 Matches 49; Conservative 44; Mismatches 84; Indels 16; Gaps 6;

QY 37 GSGDFAKSLTIRLIRCGYHVVIGSRNPK---FASEFFPHVVDVT---HEDALTKTNT 88
 Db 8 GTGNLKGKGLALRLATLGHEIVVGSRREEKAEEAKAEEYRRAGDASITGMKNEADEAACDI 67

QY 89 IFVAIIREH-YTSLWDLRHLVKGKI---LIDVSNNMRINQY--PESNAEYLASLEPDSL 141
 Db 68 AVLTPWEHAIDTARDILKNTLREKIVVSPLVPVSRGAKEYSSERSAAETVAEVLESER 127

QY 142 IVKGFRNVSAWALOLGPKDASRQVYICSNNIQARQVIELARQLNFI-PIDL 200
 Db 128 VVSALHTIPAAFRFANLDEKFDDVDPVCVGDDDESKVUMLISEIDGLRPLDAGPLNSRL 187

QY 201 IENLPPLRLFTLNR 213
 Db 188 VESLTPLILNMR 200

RESULT 6

T10120 F420-dependent NADP reductase (EC 1.6.8.-) - Methanobacterium thermoautotrophicum (strain C;Species: Methanobacterium thermoautotrophicum C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000 C;Accession: T10120 R;Berk, H.; Thauer, R.K. FEBS Lett. 438, 124-126, 1998 A;Title: F420H2:NADP oxidoreductase from Methanobacterium thermoautotrophicum: identification A;Reference number: Z16959; MUID:99037734; PMID:9821972 A;Accession: T10120 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-224 <BER> A;Cross-references: EMBL:Y17210 A;Experimental source: strain Marburg C;Superfamily: conserved hypothetical protein MJ1501 C;Keywords: oxidoreductase

Query Match 6.0%; Score 142; DB 2; Length 224;
 Best Local Similarity 29.2%; Pred. No. 0.00064; PMID:8688087
 Matches 59; Conservative 29; Mismatches 84; Indels 30; Gaps 8;

QY 37 GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVT---HEDALTKTNT 87
 Db 8 GTGDOGLGLALRAK-NKKIIGSRKEAKKAKKEILKORGIEADITGLENDAAK 66

QY 142 IVKGFRNVSAWALOLGPKDASRQVYICSNNIQARQVIELARQLNFI-PIDL 192
 Db 127 QNVIKESKVSAFQNYHAVLEDDLDNPVDCDILVCGNDDEAKKVVIDLQOIDGVRAIDC 186

QY 193 GSLSSAREIENLPLRLFTLWRGPVVVAISL 222
 Db 187 GNLEKSRTRIAIT-----PLIGINI 207

RESULT 8

F86826 hypothetical protein ygfe [imported] - Lactococcus lactis subsp. lactis (strain II1400 C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: F86826 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaiillon, O.; Malarme, K.; Weissenbach, J.; Erhart, Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: F86826 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-191 <STO> A;Cross-references: GB:AE005176; PID:g12724621; PIDN:AAK05712.1; GSPDB:GN00146 A;Experimental source: strain II1403 C;Genetics: A;Gene: ygfe

Query Match 5.1%; Score 121; DB 2; Length 191;
 Best Local Similarity 22.2%; Pred. No. 0.024; PMID:8688087
 Matches 47; Conservative 33; Mismatches 74; Indels 58; Gaps 7;

QY 32 TVGVTGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVT---HEDALTKTNT 87
 Db 3 TISIEPGKKGKMGKAI-----GDNESSSVNKVNVLNSSKTELGEI 42

QY 88 -----IIFVAIIREH-YTSLWDLRHLVKGKILDVSNMRINQYPE----SNAEYL 133
 Db 43 VVLAQPYVAAIGTIOEYSTD-----LOGKIIIDTPVDTEDSSLVPSDTSAAALI 95

QY 134 ASLFPDSLIVKGFRNVSAWALOLGPKDASRQ---VYICSNNIQARQVIELARQLNFI 189
 Db 96 AKOLPNSMIVKAFN-TTFSDTLATKVKVANEHOTTVLLASDSEAKETIKALENSGLSL 153

QY 190 IDLGSSLSSAREIENLPLRLFTL-----WRG 214
 Db 154 LDAGOSLKRARELEAIGFLOITLASEKISWDG 185

RESULT 7

D64487 hypothetical protein MJ1501 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Accession: D64487 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

RESULT 9

A;Reference number: A64300; MUID:96337999; PMID:8688087 A;Accession: D64487 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-223 <BER> A;Cross-references: GB:U67591; GB:L77117; NID:92826422; PIDN:AAB99514.1; PID:g1500389 A;Map position: REV1473617-1472946 C;Superfamily: conserved hypothetical protein MJ1501

Query Match 5.7%; Score 133; DB 2; Length 223;
 Best Local Similarity 21.9%; Pred. No. 0.0033; PMID:8688087
 Matches 46; Conservative 52; Mismatches 78; Indels 34; Gaps 7;

QY 37 GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV-----THEDALT 84
 Db 8 GTGDOGLGLALRAK-NKKIIGSRKEAKKAKKEILKORGIEADITGLENDAAK 66

QY 85 KTNITFVAIIREH-YTSLWDLRHLVKGKILDV-----SNMNRINQYPE-SNAEYL 133
 Db 67 EGDVVILSILPVEYTISTKQIKEELKGTIVSIGVPLATAIGDKPTRILLPPDGSAEMV 126

QY 134 ASLFPDSLIVKGFRNVSAWALOLGPKDASRQVYICSNNIQARQVIELARQLNFI-PIDL 192
 Db 127 QNVIKESKVSAFQNYHAVLEDDLDNPVDCDILVCGNDDEAKKVVIDLQOIDGVRAIDC 186

QY 193 GSLSSAREIENLPLRLFTLWRGPVVVAISL 222
 Db 187 GNLEKSRTRIAIT-----PLIGINI 207

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45872.1; PID:g17743615; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5183
A;Genome: plasmid

Query Match 4.9%; Score 116; DB 2; Length 198;
Best Local Similarity 22.7%; Pred. No. 0.063;
Matches 50; Conservative 41; Mismatches 81; Indels 48; Gaps 10;

QY 31 VTVGVIGSGDFAKSLTIRLRCGYHVI-GSRNPKEASEEFPV--VDVTHHEDALTKT 86
1 MTVGIGAGNIGGAFATALGKAGIEAVIANSRGPESTALVSKLGSTIRAGSVPEAAQA 60
87 NTIFVATHREHYTLSWD----LRHLLVG-KILIDVSNNMRINQY----PESNAEYLA 134
61 -INVAVAP-----WSKIPGALAGINFGDRIVIDANNSIAEAPLYRPADEGRTSDIFT 112
QY 135 SLEPPDSLIVKGENVSAWALQIGPKDAS-----ROVVICSNNIQAROQVIELARQL 185
113 ALVPGARVVKAFN-----HITPKOLSGDPHSEGGRRVLFYSGDDMRAKAEGVGAIDRI 165
QY 186 NFPIPIDLGSSISSAREIENLPLRLTLMRGPVVAISLATF 225
Db 166 GFFGIDLGGLPVGSQLQLQFP-----GGPLPAINLVKF 197

Db 157 IH-----TIERNFSVGLSFESVILWL---NKNGIQEIHNCA----- 189

RESULT 13

JN0898
follitropin receptor precursor - crab-eating macaque
N;Alternate names: follicle-stimulating hormone receptor (FSHR)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0898; S36452
R;Gromoll, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 196, 1066-1072, 1993
A;Title: Molecular cloning of the testicular follicle stimulating hormone receptor of th
A;Reference number: JN0898; MUID:94071854; PMID:7504463
A;Accession: JN0898
A;Molecule type: mRNA
A;Residues: 1-695 <GRO>
A;Cross-references: EMBL:X74454; NID:9396801; PIDN:CHA52463.1; PID:g396802
A;Note: the authors translated the codon AGT for residue 488 as Arg
C;Function:
A;Description: receptor that mediates the biochemical effects of follitropin
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat h
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein;
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-695/Product: follitropin receptor #status predicted <PFH>
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;194-218/Domain: transmembrane #status predicted <TM1>
F;367-387/Domain: transmembrane #status predicted <TM1>
F;399-421/Domain: transmembrane #status predicted <TM2>
F;444-465/Domain: transmembrane #status predicted <TM3>
F;485-508/Domain: transmembrane #status predicted <TM4>
F;529-550/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM6>
F;609-630/Domain: transmembrane #status predicted <TM7>
F;191-199,293,318/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status predicted
F;555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 4.7%; Score 111.5; DB 1; Length 695;
Best Local Similarity 17.0%; Pred. No. 0.71; Mismatches 151; Indels 183; Gaps 16;
Matches 84; Conservative 75; Mismatches 151; Indels 183; Gaps 16;

QY 79 HEDALTKTNTIFFVAIHEREHTSILWDIRHLVG-----KILIDVSNNMR 121
98 HEIRTEKANNL-LYINPEAFONLPLNRLRYLLISNTGIKHLPDVHKTHSFQKVLLDIQDNIN 156

QY 122 INQYPESNAEYLASLFPDSLIVKGFFNNSAWALQIGPKDASRQVYICSMNIQARQQVEL 181

Db 157 IH-----TIERNFSVGLSFESVILWL---NKNGIQEIHNCA----- 189

QY 182 ARQLNFIPIDLGSLSASSAREIENLPLRLTILWRGRPVVAISLATFFFLYFVRDVHYPYR 241
Db 190 ---FNGTQTLDEMLNSDNNNNLELPNDVFFHGASGPVILDISRTRIHSLPSYGLENLKIRA 246

QY 242 NQQSDFYKIPIEIVNKILPILPIVAILLISLV-----PPWLETWLOCRKQLG 306

Db 247 RSTYNLKKLP----SLEKIVVALMEASLTYPSPHCCAFANWRQOISELHPICNSKL-RQEY 301

Db 61 -INVAVAP-----LAGLLAAVQLYXGTKYRRF-----FSFIQSTLG 361

QY 302 DYMTOQTRGQRSSLAEDESNEYSYSGFDMTYAEFDYDLCNEVVDVTCSPKPDAFNPCEDILG

Db 307 ----LLSPPFAAMVHA-----YSLCLPMRMRSERYLFLNMAVQQVHANIENS 348

Db 362 YNITRVLWIWFISILAITGNNIIVLWLTTSQYKLTVP-----REFMCNLAFAD----- 408

QY 409 -----LCTIGIVILLIASDHTKSQYHNYAIDWQTGAGCDAGFFTVEASELS 456

Db 440 ---IVALLISTER-----VLIIGWKRAREEEVYRFYTPPNFV-LAL 436

Db 457 VYTITAITLERWHTITHAMQLDCKVHVRHAASVWMGWIFAFAAALFPFTGCISSYMKVI 516

QY 437 VLPSITVILDLLQL 449

Db 517 CLPMDIDSPLSQL 529

RESULT 14

S59681
probable membrane protein YPL012W - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein Ipa5w; hypothetical protein YP8132.01
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S59681; S52519
R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; W
submitted to the EMBL Data Library, August 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: S59677
A;Accession: S59681
A;Molecule type: DNA
A;Residues: 1-1228 <HAL>
A;Cross-references: EMBL:U33335; NID:g965076; PID:g965081; MIPS:YPL012W
R;Baddock, K.; Churcher, C.
submitted to the EMBL Data Library, February 1995
A;Reference number: S52519
A;Accession: S52519
A;Molecule type: DNA
A;Residues: 220-1228 <BAD>
A;Cross-references: SGD:RBP12
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:RBP12
A;Cross-references: SGD:S0005933
A;Map position: 16L
C;Keywords: transmembrane protein
F;125-141/Domain: transmembrane #status predicted <TM1>
F;478-494/Domain: transmembrane #status predicted <TM2>
F;720-736/Domain: transmembrane #status predicted <TM3>

Query Match 4.7%; Score 111.5; DB 2; Length 1228;
 Best Local Similarity 19.9%; Pred. No. 1.5;
 Matches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 28;

Qy 11 KSLSETCLPQNGINGIKDARK-----VTVGVIGSGDFAKSLSITRLI 50
 Db 292 KTMMAETTISGGLAENKVLRVLDTIFALKPSNVDTLLTKSWIAWVKGMSYATHQPLKAL 351

Qy 51 R-----CGYHWTIGSRNPKF--ASEFFPHVVDVTHHEDAL----- 83
 Db 352 RKLPGVVFHIMCTY---LASETPEVYQAASOCLISILSESVKDILLYTPSVDEKVFKNVD 408

Qy 84 -----TKTNILFVAIREHYTSILWDRHLJLJVKGKILIDVSNNMRINQYPESNAEYLASLF 137
 Db 409 EIIISQIAKTFIDPLSIRYSHCS----REIL--KILVAAFNKFY---RSNPHEFLSL 456

Qy 457 -----KIVDTWRVN-----EEOFMDIRNEIELVIGASITAMG 488
 Db 138 PDSLIVKGPNVSAWALQLGPKDASRQVYICSNNTQARQQVIELARQLNFI---- 188

Qy 189 -----PIDIGLSLSAREIENLPLRLFTLWRGPVV---VAISIATFFPLYSFVRDV 236
 Db 489 PEMILAEAPLNLDNPSSER----PGR---AWLLPLIRDYTKNANLTF-----QNEL 533

Qy 237 HYARYNQQSDFYKIPIEVN-----KTLP-----IAVITLISL 269
 Db 534 APYIJKSFQSKFDKVPEESIQLRVQFTIVDQIWSTLPRFCELPMDLRESFTDEFASELSSL 593

Qy 270 VYL-----AGLLAAAYQLYYGTK-----YRRFP-----PWLETWLQCRK 303
 Db 594 LYSEVELRTTICHAIKVLAESNVSYAEESSHNVLLQRFPISEACKNEYLT----K 648

Qy 304 QIGLISFFEFAMVHAYSLCIPMRS-----ERYL-----FLNAYAOQVHANIENSWE 351
 Db 649 STNLALAVLFNV----YTQTPNARSYILETIDQYKLITSKEDLEKTFNNVCGLLKNMNE 704

Qy 352 HEVWRRIEMVYISFGIMSLGLLIL--AVTISIPSVSNALNWREFSFIQSTLGIVALLISTFH 409
 Db 705 ESSGNVNKEKKKPQLTATLDDLCIMITYLPVSSYSAFLSMFS-----LTVNSAD 754

Qy 410 VLIYGWKRAFEEYYRFYT 428
 Db 755 ALIQ---KRA-----YRIT 766

RESULT 15
 B84410 hypothetical Protein Vng2607c [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Accession: B84410
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; PMID:20504483; PMID:11016950
 A;Accession: B84410
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-222 <STOP>
 A;Cross-references: GB:AE004437; NID:910581987; PIDN:AAG20646.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG2607C
 C;Superfamily: conserved hypothetical protein MJ1501

Db 8 GTGDIGAGIALRWATSDHDIVIGSRDPEKARETAAYEDTLADQGVDRKLITGFANEMA 67
 Qy 84 TKTNTIFVAIREHYTSILW-----DRHLJLJVKGKILIDVSNNMRINQYPESNAEYL 133
 Db 68 DRADWVVAVPAYHVTDVNGAVADRLADTIVSPAVGIASGEHGLHYNPPSAGSVTALV 127
 Qy 134 ASLFPDSL-TVKGFNVVSAWALQLGPKDASRQVYICSNNTQAROOVIELARQLNFI-PID 191
 Db 128 ADAAPDGDVVGAFHNLADRLADLDTELDADTIVVGNDEGARTRVAAELADDITGLRALD 187

Db 192 LGSISSAREIENLPLRLFTLWR 213
 Qy 188 AGPVENAAEVESLTPLLINLAR 209

Search completed: March 2, 2004, 06:12:46
 Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 20:23:21 ; Search time 45 Seconds
(without alignments)
520.849 Million cell updates/sec

Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESTISMMGSPKSLSITCIPN.....ALVLPSTIVILDILQLCRYPD 454
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued patents AA:*

1: /cggn2_5/ptodata/2/iaa/5A_COMB.pep: *
2: /cggn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cggn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cggn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cggn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
6: /cggn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	901	38.3	173	4 US-09-323-873A-8
2	736	31.3	141	3 US-09-083-521-1
3	717	30.5	339	4 US-09-323-873A-2
4	717	30.5	339	4 US-09-685-166A-879
5	144.5	6.1	227	4 US-09-655-270A-15
6	144.5	6.1	227	4 US-09-651-941-17
7	144.5	6.1	227	4 US-09-955-597-17
8	107.5	4.6	695	1 US-08-487-886-2
9	107.5	4.6	695	3 US-08-482-855-2
10	107.5	4.6	695	4 US-08-474-986-2
11	107	4.6	34	4 US-09-323-873A-20
12	102.5	4.4	940	4 US-09-328-352-8165
13	101	4.3	476	3 US-09-316-083-3
14	101	4.3	476	3 US-09-933-700-3
15	101	4.3	724	4 US-09-252-991A-21494
16	99	4.2	365	4 US-09-170-496D-118
17	99	4.2	365	4 US-09-170-496D-226
18	99	4.2	365	4 US-09-364-425B-27
19	99	4.2	531	2 US-08-724-974A-2
20	97.5	4.1	390	3 US-08-460-576-2
21	97	4.1	692	3 US-07-757-342D-6
22	97	4.1	692	4 US-09-461-657B-6
23	96	4.1	299	4 US-09-903-456-61
24	96	4.1	1309	4 US-09-975-413A-10
25	94.5	4.0	288	4 US-09-107-532A-6009
26	94.5	4.0	296	4 US-09-540-236-2922
27	94.5	4.0	345	4 US-09-489-039A-10740

ALIGNMENTS

RESULT 1	US-09-323-873A-8
; Sequence 8, Application US/09323873A	
; Patent No. 6329503	
; GENERAL INFORMATION:	
; APPLICANT: Daniel E. Afar	Rene S. Hubert
; APPLICANT: Kahn Leong	
; APPLICANT: Arthur B. Raitano	
; APPLICANT: Douglas C. Saffran	
; APPLICANT: Steve Chappell Mitchell	
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS	
; FILE REFERENCE: EXPRESSED IN HUMAN CANCERS AND USES THEREOF	
; CURRENT APPLICATION NUMBER: US/09/323,873A	
; PRIOR APPLICATION NUMBER: 60/091,183	
; PRIOR FILING DATE: 1998-06-01	
; CURRENT FILING DATE: 1999-06-01	
; NUMBER OF SEQ ID NOS: 32	
; SOFTWARE: FastSEQ for Windows Version 4.0	
; SEQ ID NO 8	
; LENGTH: 173	
; TYPE: PRT	
; ORGANISM: Homo Sapiens	
US-09-323-873A-8	
Query Match	38.3%; Score 901; DB 4; Length 173;
Best Local Similarity	100.0%; Pred. No. 1.4e-86; Mismatches 0; Indels 0; Gaps 0;
Matches 173; Conservative	
QY	246 DFYKIPRIETVKTLPIVATITLISIVLAGLAAAYQLYGTYRKYRFPWLLETWLOCRKQL 305
Db	1 DFYKIPRIETVKTLPIVATITLISIVLAGLAAAYQLYGTYRKYRFPWLLETWLOCRKQL 60
QY	306 GLLSFFFAMVHAYSLCLPMRRSERVLFLNMAYQVQHANIENSWEENEWRIEMYISFGI 365
Db	61 GLISFFPMVHAYSLCLPMRRSERVLFLNMAYQVQHANIENSWEENEWRIEMYISFGI 120
QY	366 MSLGLISLLAVTSIPSVAALNWREFSFICSTLGVALLISTFHVLIVGKRA 418
Db	121 MSLGLISLLAVTSIPSVAALNWREFSFICSTLGVALLISTFHVLIVGKRA 173
RESULT 2	
US-09-083-521-1	
; Sequence 1, Application US/09083521	
; Patent No. 6048970	
; GENERAL INFORMATION:	

APPLICANT: Guebler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-323-873A-2

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/M
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,521
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

; CLONE: 1691243
US-09-083-521-1

Query Match	Score	DB	Length
Best Local Similarity	100.0%	Pred. No.	2.2e-69;
Matches	141;	Conservative	0;
Mismatches	0;	Indels	0;
Gaps	0;		
Qy	314	MVHVAYSLCLPMRRSERYLFLNMAVOVHANIENSNEEVWRIEMYISFGIMSLGLSL	373
Db	1	MVHVAYSLCLPMRRSERYLFLNMAVOVHANIENSNEEVWRIEMYISFGIMSLGLSL	60
Qy	374	LAVTSIIPSVSNALNWREFSFISTLGVALLISTFHVLIGWKRAFEEEYVREVTPPNV	433
Db	61	LAVTSIIPSVSNALNWREFSFISTLGVALLISTFHVLIGWKRAFEEEYVREVTPPNV	120
Qy	434	LALVLPSPIVLDLLQLCRYPPD	454
Db	121	LALVLPSPIVLDLLQLCRYPPD	141

RESULT 3
US - 09 - 323 - 873A - 2
; Sequence 2, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323, 873A
CURRENT FILING DATE: 1999-06-01

Db 67 LFPQWHLPIKIAIASLTFLYTLREVIHPLATSHQQFYKI PILVINKVLPMVSITLL 126

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 17

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Rhodococcus erythropolis HL PM-1

US-09-651-941-17

Qy 268 SLVYLGLLAAAYQLYKGTKYRFPFWLETWLQCRQKOLGLLSFFPAMVHWAWSLCLPMRR 327

Db 127 ALVYLPGVIAAIVOLNGTKYKFPFWLKDMLTRKQFGLSFFAVLHAIYSLSYPMRR 186

RESULT 5

US-09-655-270A-15

; Sequence 15, Application US/09655270A

; Patent No. 6329151

; GENERAL INFORMATION:

; APPLICANT: Rouverie, Pierre E.

; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic mRNA

; FILE REFERENCE: BC1011 US NA

; CURRENT APPLICATION NUMBER: US/09/655, 270A

; CURRENT FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/120, 702

; PRIOR FILING DATE: 1999-February-19

; PRIOR APPLICATION NUMBER: 60/152, 542

; PRIOR FILING DATE: 1999-September-03

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 15

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Rhodococcus erythropolis HL PM-1

Query Match 6.1%; Score 144.5; DB 4; Length 227;

Best Local Similarity 28.0%; Pred. No. 6.4e-07;

Matches 60; Conservative 33; Mismatches 88; Indels 33; Gaps 9;

Patent No. 6329151

Qy 388 WREPFSPFIOSTLGIVALLISTFHVLITYGWKRAFEELYRFXTPPNPFVIALVLP\$IVIL 444

Db 187 SYRYKLINWAYQQVOONKEDAWIEHDVWRMEIYVSLGIVGLAILLAVTSIPSVDSDLT 246

Qy 247 WREPFHYIQSKLGIIVSLLGTTIHALIFAWNWKIDIKQFVWYTPPTFMAILAVELPIVWL 303

Qy 76 VTHHEDALTAKTNITFVAL---HREHYTSLWDLRHLVGKILL-----DVSNMRIN 123

Db 59 AADNASAADCPILLWVPYDGHREJVS---ELAPIFACEKLWVSCYNPLGFDSGAYGLD 115

Qy 124 QYPESNAEYLASLFPDSSLIVKGFNWVA---WALQLGPKDASRQVYICSNNIQARQVTE 180

Db 116 VEEGSAAEQRLDIVPGATVVAFAFHHLISAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172

Qy 181 LARQLNFIPI-DLGSLSARETENLPLRLFTLWR 213

Db 173 LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206

RESULT 7

US-09-955-597-17

; Sequence 17, Application US/09955597

; Patent No. 6461856

; GENERAL INFORMATION:

; APPLICANT: ROUVIER, PIERRE E

; APPLICANT: WALTERS, DANA M

; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation

; FILE REFERENCE: BC1022 US NA

; CURRENT APPLICATION NUMBER: US/09/955, 597

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: 60/152, 545

; PRIOR FILING DATE: 1999-10-03

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 17

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Rhodococcus erythropolis HL PM-1

Query Match 6.1%; Score 144.5; DB 4; Length 227;

Best Local Similarity 28.0%; Pred. No. 6.4e-07;

Matches 60; Conservative 33; Mismatches 88; Indels 33; Gaps 9;

Patent No. 6461856

Qy 76 VTHHEDALTAKTNITFVAL---HREHYTSLWDLRHLVGKILL-----DVSNMRIN 123

Db 59 AADNASAADCPILLWVPYDGHREJVS---ELAPIFACEKLWVSCYNPLGFDSGAYGLD 115

Qy 124 QYPESNAEYLASLFPDSSLIVKGFNWVA---WALQLGPKDASRQVYICSNNIQARQVTE 180

Db 116 VEEGSAAEQRLDIVPGATVVAFAFHHLISAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172

Qy 181 LARQLNFIPI-DLGSLSARETENLPLRLFTLWR 213

Db 173 LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206

RESULT 6

US-09-651-941-17

; Sequence 17, Application US/09651941

; Patent No. 6355470

; GENERAL INFORMATION:

; APPLICANT: ROUVIER, PIERRE E

; APPLICANT: WALTERS, DANA M

; APPLICANT: RAINER, RUSS

; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation

; FILE REFERENCE: BC1022 US NA

; CURRENT APPLICATION NUMBER: US/09/651, 941

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 60/152, 545

; PRIOR FILING DATE: 1999-10-03

; NUMBER OF SEQ ID NOS: 28

Qy 25 IKDARKVTGVIGSGDFAKSLTIRLRCGYHVWVIGSRNPFASEEFFPH-----VWD 75

Db 1 MKSSKIAWVG--GTGPQGKGLAYRFAAGWPWVIGSRSAAEAALEVRERRAGDGAVVS 58

Qy 76 VTHHEDALTAKTNITFVAL---HREHYTSLWDLRHLVGKILL-----DVSNMRIN 123

Db 59 AADNASAADCPILLWVPYDGHREJVS---ELAPIFACEKLWVSCYNPLGFDSGAYGLD 115

Qy 124 QYPESNAEYLASLFPDSSLIVKGFNWVA---WALQLGPKDASRQVYICSNNIQARQVTE 180

Db 116 VEEGSAAEQRLDIVPGATVVAFAFHHLISAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172

Qy 181 LARQLNFIPI-DLGSLSARETENLPLRLFTLWR 213

Db 173 LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206

RESULT 8

US-08-487-886-2

; Sequence 2, Application US/08487886
; Patent No. 574448
; GENERAL INFORMATION
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 574448een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Mass1 via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487, 886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670, 085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 228546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -17 to -1
; IDENTIFICATION METHOD: hydrophobic
; FEATURE:
; NAME/KEY: putative amino-terminal extracellular domain
; LOCATION: 1 to 349
; IDENTIFICATION METHOD: similarity with other receptor extracellular
; IDENTIFICATION METHOD: dimeric glycoprotein
; IDENTIFICATION METHOD: domains, hydrophilic
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 350 to 613
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane domains
; FEATURE:
; NAME/KEY: putative transmembrane region I
; LOCATION: 350 to 370
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region II
; LOCATION: 382 to 404
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region III
; LOCATION: 427 to 448

IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region IV
; LOCATION: 469 to 491
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region V
; LOCATION: 512 to 533
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VI
; LOCATION: 557 to 580
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VII
; LOCATION: 592 to 613
; IDENTIFICATION METHOD: similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative carboxy-terminal intracellular domain
; LOCATION: 614 to 678
; US-08-487-886-2

Query Match 4.6%; Score 107.5; DB 1; Length 695;
Best Local Similarity 17.0%; Pred. No. 0.028; Matches 84; Conservative 77; Mismatches 148; Indels 185; Gaps 17;
Db QY 79 HEDALIITKTNIFVVAIHRHRTSLWDLRHLVG-----KILIDVSNNMR 121
Db 98 HEIRIEKANNL-LYINPEAFQNLPNLQYLISNTGIKHLPLDVHKIHSIQVLDIQDN 156
Db QY 122 INQYPESNAEYLASLFPDSLIVKGENTVSAWALQOLGPKDASRQVWICSNNIQAROOVIEL 181
Db 157 IH-----TIERNSFVGLSFESVILWL---NKNQGIEHNC----- 189
Db QY 182 ARQLNFIPIIDLGSLSLSSAREIENIPLRLFTLWRGRPVVAISLATFFFLYSFVRDVHRYAR 241
Db 190 ---FNGTQDLENLSDNNNLLEELPNDVFGASGPVILDISRTIRHSIPLSYGLENLKLRA 246
Db QY 242 NQQSDFYKIPIEIVNKTL-PIVAILLISLV-----PPWLETWLOQORKQL 305
Db 247 RSTYNLKRLP-----TELEKLVALMEASLTYPSSHCCAFANWRROQISELHPICKNSKILRQE 300
Db QY 272 -----LAGLLAAQYLYGKTYRRF-----PPWLETWLOQORKQL 305
Db 301 VDYMTOQTGCRSSLAEDNESSYSRGFDMDTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM 360
Db QY 306 G----LLSFFFAMVHA-----YSLCLPMMRRSERYLFNMAYQVHANIEN 347
Db 361 GYNILRVLWIFSLAITGTNTIVLVLITTSQYKLTVP----RFLMCNLAFAD---- 408
Db QY 348 SWNEEEVWRIEWYISFGIMSLIGLSSLAVTSIPSVSNALNRE-----FSFIQSTL 398
Db 409 -----ICIGIYILLIASVDIHTKSQYHNVYADWQTGAGCDAAGFFTVFASEL 455
Db QY 399 G----WALLISTFH-----VLIYGMKRAFEEEYRFYTRPNFY-LA 435
Db 456 SVYTTAITLEWRWTITHAMQLDCKVQLRHAASWVNGWIAFAAALFPPIFGISSYMKVS 515
Db QY 436 LVLPSPIVLDLQL 449
Db 516 ICLPMDIDSPLSQL 529

RESULT 10
US-08-474-986-2
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 637271ileen Patrice
TITLE OF INVENTION: Human Follicle Stimulating
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546

REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
LOCATION: 614 to 678

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-474-986-2

Query Match 4.6%; Score 107.5; DB 4; Length 695;
Best Local Similarity 17.0%; Pred. No. 0.028;
Matches 84; Conservative 77; Mismatches 148; Indels 185; Gaps 17;

QY 79 HEDALTTKTMILFVVAIRHEHTISLWIDLRHLLVG-----KILLDVSNMR
Db 98 HEIRIEKANNL-LYINPEAFONLPLNLQYLLISNTGKHLPDVHKTHSLOKLVIDODNIN 156

QY 122 INQYEPESNAEYLASLFPDSLIVKGFTNWSAWALQLGPDKDASRQVYICSNNIQARQVIEL 181

Db 157 IH-----TIERNSFGVGLSPESVILWL---NRNGIQEIHNC----- 189

QY 182 ARQLNFIPIIDLGSLSAREIENLPLRLFTLWRGPVVVAISLATFFFLYFVFRDVHYPAR 241

Db 190 ---FNGTQDDEINLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLOPSYGLEMLKKLA 246

QY 242 NQQSDPYKIPIEIVNKTL-PIVATLISLV----- 271

Db 247 RSTYNLKKLP-----TEKLVALMEASLTYPHCCAFFANWRROQISELHPICKNSILRQE 300

QY 272 -----LAGLIAAYQLYXGTKRYRF-----PPWLETWLOCRKQ 305

Db 301 VDYMTOQRGQRSSLAEDNESSYSRGFDMDTYEFDYDLCNEVVDVTCSPKDAFNPCEDIM 360

QY 306 G-----LISFFFAMVHVA-----YSICLPMRSERYFLINMAYQQHANTEN 347

Db 361 GYNILRVLWIFISILAITGNITIVLVLTTSQYKLTV----- 408

RESULT 11
US-09-323-873A-20
Sequence 20, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Douglas C. Saffran
APPLICANT: Kahar Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chapell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.160SU2

CURRENT APPLICATION NUMBER: US/09/323, 873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 34

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: STEAP-1 PEPTIDE
US-09-323-873A-20

Query Match 4.6%; Score 107; DB 4; Length 34;
Best Local Similarity 58.8%; Pred. No. 0.0003;
Matches 20; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 326 RRSERYFLINMAYQOQNENIENSNEEVRIEM 359
Db 1 RRSVRYKLINWAOQQQDNKEDAWIEHDVWREI 34

RESULT 12
US-09-328-352-8165
; Sequence 8165, Application US/09328352
; Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8165
LENGTH: 940
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-8165

Query Match 4.4%; Score 102.5; DB 4; Length 940;
Best Local Similarity 19.5%; Pred. No. 0.15;
Matches 71; Conservative 74; Mismatches 146; Indels 73; Gaps 17;

QY 88 IFVVAIHRHYSIWLWDURHILVGKILIDVSNNMRINQYPESSNAEYLASL----FPDLSI 142
 Db ::|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|:
 Db VFLTLVFSHHFGV--ITSLTASILFTILLAITVFLSLKQQAIYIALALGMAYAAPLV 319
 QY 143 VKGF--NVSAWALQLGPKDASRQVYICSNNIQAROQVIELAROLN---FIPIDLGSLS 196
 Db :|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|:
 QY 320 IPQRPDVFLS-----YVLVNLAVAANFIOPWKILNQIAFFATMFIGSA 368
 Db |: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|: ;|:
 QY 197 SAREIENPLRLFTL-WRGPVVVAISLATFFLYSFVRDVHYPARNQSDFYKIPIEV 255
 Db 369 IAFYAE--PAKFDTLDW---ILWLHALFTLWSVRYSONISRVSHEKOEGIRLP---
 Db 256 NKTLPIVAITLISLVLAGLLAAVQLYYGTK-----YRFPWPMLTWLQCRK 303
 QY 419 ---PLDVGGLIFNVPGVLFITLHAYLVESTQALTIGAAGLTYAVLTIEWIK--KTHP 471
 Db 304 QIGLISFFAMVHA-YSLCLPMMRRSERYLFLNMAYQVHANIENSNEEVRIEMVIS 362
 QY 472 QLSVLAKSFFILAVAFFALIFPLAKGAHWTAGWVAOGTALIV--WGYTERYRLSRV- 527
 Db 363 PGIMSLGILSLLAUTSIPSVSNALNW--REFSFIQSTLGIVALLISTPHVLIYGMKRAFE 420
 QY 528 -GVVILVLLSSLALFYQV-----WANEEFPTLSTSIVATAQFISAFYVLOQNSK--E 575
 Db 421 EYV 424
 QY 576 QRVF 579

RESULT 13
 US-09-316-083-3
 ; Sequence 3, Application US/09316083A
 ; Patent No. 6280942
 ; GENERAL INFORMATION:
 ; APPLICANT: The Institute of Physical and Chemical Research
 ; TITLE OF INVENTION: Endonuclease
 ; FILE REFERENCE: PH-651
 ; CURRENT APPLICATION NUMBER: US/09/316, 083A
 ; CURRENT FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: JPP98/141861
 ; EARLIER FILING DATE: 1998-05-22
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 476
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-316-083-3

Query Match 4.3%; Score 101; DB 3; Length 476;
 Best Local Similarity 20.7%; Pred. No. 0.075; Mismatches 85; Indels 66; Gaps 12;
 Matches 52; Conservative 48; Mismatches 85; Indels 66; Gaps 12;

QY 62 NPKFASEFPHTVDVTHEDALTNTN---IFVAIHRHYSIWLWDURHILVGKILIDVSNNMRINQYPESSNAEYLASL--PDSLIVKGPNVWSAWALQLGPKD 161
 Db 254 NPYFVNAPSINTI-----KTNLAKEKIFTNINYNKLYSDYKINOINNNHIPPYNYLK 302
 QY 104 LRHLIVGKILIDVSNNMRINQYPESSNAEYLASL--PDSLIVKGPNVWSAWALQLGPKD 161
 Db 303 INNKLPPIKNMDIKNNYWLAGFTAADGFSFLSSWNPKDTLFLFKNM----- 347
 QY 162 SROQVYICSNNIQAROQVIELAROLNFIPIIDLGSLSAREIENPLRLFTLWRGPVVAIS 221
 Db 348 -RPSYVVIS-QVETRKELIYLIQE---SFDL-SISNVKKVGNRKLKDFFLFRTRTTDELMK 400
 QY 222 LATFFFLYSFVRDVHYPARNQSDFYKIP---IEIVNKTLPIVAITLISLVLAGLLA 277
 Db 401 ----FIVYF--DKFLPLHDNQFNYIKFRFNTFFIKSYNNWNRVFGVLVSE--YINNIKI 451
 QY 278 AAYQLYYGTK 288
 Db 452 DNYDYYYNKY 462

RESULT 15
 US-09-252-991A-21494
 ; Sequence 21494, Application US/09252991A
 ; Patent No. 6551795
 ; General Information:
 ; Applicant: Marc J. Rubenfield et al.
 ; Title of Invention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; File Reference: 107196.136
 ; Current Application Number: US/09/252, 991A
 ; Current Filing Date: 1999-02-18
 ; Prior Application Number: US 6,0/074, 788
 ; Prior Filing Date: 1998-02-18
 ; Prior Application Number: US 6,0/094, 190
 ; Prior Filing Date: 1998-07-27
 ; Number of Seq ID Nos: 33142
 ; Seq ID No 21494
 ; Length: 724
 ; Type: PRT
 ; Organism: Pseudomonas aeruginosa
 ; US-09-252-991A-21494

Query Match 4.3%; Score 101; DB 4; Length 724;
 Best Local Similarity 20.5%; Pred. No. 0.14; Mismatches 105; Indels 118; Gaps 16;

QY 222 LATFFFLYSFVRDVHYPARNQSDFYKIP---IEIVNKTLPIVAITLISLVLAGLLA 277
 Db 401 ----FIVYF--DKFLPLHDNQFNYIKFRFNTFFIKSYNNWNRVFGVLVSE--YINNIKI 451
 Db 452 DNYDYYYNKY 462

QY 132 YLASLFPDSLIVKGPNVSAWALQLGPKDASRQVVICNNIQA---RQQVIBAROLN 186
 Db 298 YLSVVLPDSL-SKTLAMMAYVTLVCGTILFSA---LCVLSLISLSPHRQRALDILRRQA 352
 QY 187 FIPIDL-GSLSARETIENPLRLIFTLWRGPVVVAISLA---TFFFLYSFVRDVH 238
 Db 353 FRPLWLIGSLAAIGEVAHDPRLIAGLGEHTSICLSTLANASAALFTALFVMRFRPTAH- 411
 QY 239 YARNQO--- SDFYKIP 412 LIRNQPLERRIKRSIHDIVQLWSIWFVYPLVLWGISLFATFVSAGDSSALARLYCA 471
 Db 412 LIRNQPLERRIKRSIHDIVQLWSIWFVYPLVLWGISLFATFVSAGDSSALARLYCA 471
 QY 258 TLPIVAITLISLYLAGLLAAYQLYGTYKRRPPWLETWLLOCKRQLGLLSFFFAMVHV 317
 Db 472 VLAVVAMTVIGHI-----RRRSSRGAGPRRSAPYIEQ-----LQSFGYTILHT 515
 QY 318 AYSLCLPMRRSERVLFNMAVQQVHANIENSNEEEVWRIEM-YISFGIM--- 366
 Db 516 FVVL-----FFIEVALRVWGMSLIR-YAEGEQEISMKVVSFGTTLIVAWLIWIL 564
 QY 367 -----SGLI-----LSLLAVTSIPSVSNALNWREFPSFIOSTLGYVALLIS 406
 Db 565 TDTAIQHSIGLGGKSHPNTRALTMILPRLRVNL-----FATIAVIALIVA 608

Search completed: March 1, 2004, 23:40:58
 Job time : 48 secs

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Gencore version 5.1.6

OM protein - protein search, using sw model

Perfect score: US-09-455-486-6

Run on: March 1, 2004, 19:51:19 ; Search time 40 Seconds
 (without alignments)
 59.996 Million cell updates/sec

Sequence: 1 MESISMMGSPKSLSETCLPN.....ALVPSIVILDLLQLCRYPD 454

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	717	30.5	339	1	STEAP_HUMAN	Ogube8 homo sapien
2	133	5.7	223	1	F4RE_METJA	Q58896 methanococc
3	120.5	5.1	232	1	F4RE_METTH	Q26350 methanobact
4	111.5	4.7	695	1	FSHR_MACFA	P32212 macaca fasc
5	109.5	4.7	206	1	Y538_PASMU	Q9cm97 pasteurella
6	109	4.6	693	1	FSHR_CHICK	P79763 gallus gall
7	109	4.6	712	1	FRE6_YEAST	Q12473 saccharomy
8	107.5	4.6	629	1	FRE7_YEAST	Q12333 saccharomy
9	107.5	4.6	695	1	FSHR_HUMAN	P23945 homo sapien
10	104.5	4.4	695	1	FSHR_PIG	P49059 sus scrofa
11	104	4.4	396	1	SOTB_ECOLI	P58529 escherichia
12	104	4.4	396	1	SOTB_ECOLI	P31122 escherichia
13	103	4.4	465	1	NPT1_MOUSE	Q61983 mus musculu
14	102.5	4.4	391	1	NUCC_NEPOL	Q9tkv6 nephroselmi
15	102	4.3	220	1	Y304_BRUME	Q8yd73 brucella me
16	102	4.3	220	1	Y3J1_BRUSU	Q8fv59 brucella su
17	100	4.3	476	1	RF3_SACBA	P05512 saccharomy
18	99.5	4.2	452	1	NU4M_BRALA	Q79421 branchiosto
19	99	4.2	365	1	SPR1_HUMAN	Q15743 homo sapien
20	98	4.2	3411	1	POLG_YEFV1	P03314 y genome po
21	98	4.2	3411	1	POLG_YEFV2	P19901 y genome po
22	97.5	4.1	268	1	YD49_AQUAE	O67364 aquifex aeo
23	97.5	4.1	695	1	FSHR_BOVIN	P35376 bos taurus
24	97	4.1	218	1	YGA6_XANAC	Q8ply9 xanthomonas
25	97	4.1	692	1	FSHR RAT	P20395 rattus norv
26	96.5	4.1	686	1	FRE1 YEAST	P32791 saccharomy
27	96	4.1	261	1	PHSC_ECOLI	P77409 escherichia
28	95	4.0	202	1	YAJ1_PSEAE	O9hva5 pseudomonas
29	95	4.0	393	1	NUCC_ARATH	P56753 arabidopsis
30	95	4.0	393	1	NUCC_SPIOL	Q9m3is spinacia ol
31	95	4.0	692	1	FSHR MOUSE	P35378 mus musculu
32	94.5	4.0	492	1	SBCY_CYAPA	P25014 cyanophora
33	94.5	4.0	695	1	FSHR SHEEP	P35379 ovis aries

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CC -!- FUNCTION: Catalyzes the reduction of F420 with NADP(+) and the reduction of NADP(+) with F420H(2). Probably couples the NADP-dependent oxidation of the alcohol to the aldehyde with the F420-dependent reduction of CO(2) to methane (anabolic function) (By similarity).

CC -!- CATALYTIC ACTIVITY: NADPH + coenzyme F420 = NADP(+) + reduced coenzyme F420.

CC -!- SIMILARITY: TO M.ORGANOPHILUM F420-DEPENDENT NADP REDUCTASE.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AE000811; AAB84754; 1; -.

CC DR PIR; A69131; A69131.

CC DR InterPro; IPR04455; NADPoxred_F420.

CC Pfam; PF03807; F420_oxidored; 1.

CC DR TIGRFAMS; TIGR00301; TIGR00301; 1.

CC KW Hypothetical protein; Oxidoreductase; NADP; Complete proteome.

CC SQ SEQUENCE 232 AA; 24539 MW; AICE60ABC8474296 CRC64;

Query Match 5.1%; Score 120.5; DB 1; Length 232;

Best Local Similarity 23.8%; Pred. No. 0.029; Mismatches 90; Indels 25; Gaps 6;

Matches 49; Conservative 42; Mismatches 90; Indels 25; Gaps 6;

OY 3.0 KVTVGVIGSGDFAKSLTIRLIRCGYHVVGSRNPKEASFFPHVVDVTHHE----- 80

Db 8 KIAV-IGGTGQGLGLALRPAVAGEEVIGSRAEKASKVLEIAGRDDISVEGATN 66

OY 81 -DALTKTNIIIFVAIH-REHYTSIWLDRHLVKGKILIDS-----NNMRINQYPESN 129

Db 67 PDAASADWVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS 126

OY 13.0 AEYLASLF---PDSLIVKGFNVWSAWALQLGPDKDASRQVYICSNNIQARQQVIELARQLN 186

Db 127 AAERAARFIREQGTRVAAAFNNISASALLEVSEPVDCDCLVASDHRALEVAELAEKID 186

OY 187 FT-PIDLGSLSASSAREIENLPLRLFTL 211

Db 187 GVRAIECGGGLENARIEEKITPLLLN 212

RESULT 4

FSHR_MACFA_ID	FSHR_MACFA_STANDARD	PRT	695 AA.
AC P32212;			
DT 01-OCT-1993 (Rel. 27, Created)			
DT 01-OCT-1993 (Rel. 27, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last annotation update)			
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).			
DE FSH-R.			
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrini; Cercopithecidae; Cercopithecinae; Macaca.			
OC NCBI_TaxID=9541;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Testis;			
RX MEDLINE=94701854; PubMed=7504463; Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.; "Molecular cloning of the testicular follicle stimulating hormone receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis."; Biochem. Biophys. Res. Commun. 196:1066-1072(1993).			
CC -!- FUNCTION: Receptor for follicle stimulating hormone. The activity of this receptor is mediated by G proteins which activate adenylylate cyclase.			

Query Match 4.7%; Score 111.5; DB 1; Length 695;

Best Local Similarity 17.0%; Pred. No. 0.56; Mismatches 151; Indels 183; Gaps 16;

Matches 84; Conservative 75; Mismatches 151; Indels 183; Gaps 16;

OY 79 HEDALTKNIIIFVAIHREHTSLWDLRHLVKGKILIDS-----NNMRINQYPESN 121

Db 98 HEIRIEKANNL-LYINPEAQNLPNLRLYLLSNTGKHLPDWKHSFQKVLLDQIN 156

OY 122 INQYPESNAEYLASLFPSLIVKGFNVWSAWALQLGPDKDASRQVYICSNNIQARQQVIEL 181

Db 157 IH-----TIERNSFVGLSFESVILW---NKNGIQETINCA----- 189

OY 182 ARQLNFIPIIDLGSLSASSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHYPAR 241

Db 190 ---FNGTQLDDELNLSDNNNTEELPLNDVFHGASGPVIDISRTRIHSLSYGLENLKLR 246

Query Match 4.7%; Score 109.5; DB 1; Length 206;
 Best Local Similarity 23.8%; Pred. No. 0.18;
 Matches 56; Conservative 44; Mismatches 72; Indels 63; Gaps 13;

QY 242 NQQSDFYKIPIEIVNKTLPIVAILLISLVY 271
 Db 247 RSTYNLKKLP---SLEKLVALMEASLTYPISHCCAFFANWRQISELHPICNKSILRQE 301
 QY 272 -----LAGLLAAAYQOLYYGTYKRF-----PPWLETWLOCKRQOLGLISFFRAMVHAYSLCLPMRRSERYLEFLN 335
 Db 302 DYMTQTRGQRSSLAEDNESSYSRGFDMDTYAEFDYDLCNEVVDVTCSPKPDAFNPCEDIG 361
 QY 307 -----LISFFFAMVHVA-----YLCLPMRSERVLFLNMAQQVHANIENS 348
 Db 362 VNLLRVLINFIISILAITGNITVLTTSQYKLTVP----RFLMCNLAFAD---- 408
 QY 349 WNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNRE----FSFIQSTLG 399
 Db 409 -----LCIGIYILLIASVDIHTKSQYHNYAIDWQTGAGDAAGEFFTVEASELS 456
 QY 400 ---YVALLISTFH-----VLIYGKRAFEEEYVRFYTPPNFV-LAL 436
 Db 457 VYTLLTAITLERWHTITHAMQLDCKVHVRHAASVMMGWIFAFAALEPPIFGISSYMKVSI 516
 QY 437 VLPSIVILDLLQI 449
 Db 517 CLPMDIDSPSQL 529

RESULT 5
 Y538_PASMU STANDARD; PRT; 206 AA.
 ID Y538_PASMU STANDARD; PRT; 206 AA.
 AC Q9CN97;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein PM0538.
 GN PM0538.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li J.J., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of *Pasteurella multocida* Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the UPF0191 family.
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 CC
 DR EMBL; AE006089; AAK02622.1; -.
 DR HAMAP; MF_01207; -; 1.
 DR InterPro; IPR007916; UPF0191.
 DR Pfam; PF05252; UPF0191; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 7 26 POTENTIAL.
 FT TRANSMEM 41 63 POTENTIAL.
 FT TRANSMEM 76 98 POTENTIAL.
 FT TRANSMEM 113 135 POTENTIAL.
 FT TRANSMEM 142 164 POTENTIAL.
 FT TRANSMEM 169 191 POTENTIAL.
 SQ SEQUENCE 206 AA; 23653 MW; 2F27729D7F11194 CRC64;

QY 228 LYSFVRDVH-----PYA-----RNQSDFYKIPIEIVNKTLPIVAILLISLVY 275
 Db 1 MLSLFRIIHVCCCLGPVAVLWLLSGDESQQLGADPIKEI0HFLGFSELIMFILG- 59
 QY 276 LAAYOLYYGTYKRF-----PPWLETWLOCKRQOLGLISFFRAMVHAYSLCLPMRRSERYLEFLN 335
 Db 60 -----KVYLLK---QPOLOV---LRALGLWAFLVYVLLHV-YA-----YLAE 96
 QY 336 MAYQQVHANIENSWNNEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNRE 395
 Db 97 LGYD-----FSLFVQELVNR--GYLIIGAIATLILTMALSSWSYLK--LKGKWWFYL 146
 QY 396 STLGVALLISTFHVLITYGKRAFEEEYVRFYTPPNFVLAVALVLPSTIVTDLIQLC 450
 Db 147 HQIGYVALLLGATH--YVW-----SVKNVTFSSML--YIILSIMILC 184

RESULT 6
 FSHR_CHICK STANDARD; PRT; 693 AA.
 ID FSHR_CHICK STANDARD; PRT; 693 AA.
 AC P79763; Q90719;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 GN FSHR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata;Vertebrata; Buteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=97473503; PubMed=9332357;
 RA Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Mizuno S.;
 RT "The cDNA cloning and transient expression of a chicken gene encoding
 a follicle-stimulating hormone receptor.";
 RL Gene 197:121-127(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn;
 RX MEDLINE=97057887; PubMed=8902217;
 RA You S., Bridgeman J.T., Foster D.N., Johnson A.L.;
 RT "Characterization of the chicken follicle-stimulating hormone
 receptor (cFSH-R) complementary deoxyribonucleic acid, and expression
 of cFSH-R messenger ribonucleic acid in the ovary.";
 RL Biol. Reprod. 55:1055-1062(1996).
 CC This receptor for follicle stimulating hormone. The activity
 of this receptor is mediated by G proteins which activate
 CC adenylate cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
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 CC
 DR EMBL; D87871; BAA13487.1; -.
 DR InterPro; IPR001611; LRR.
 DR HSSP; P23945; 1XUN.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR Pfam; PF00001; 7tm_1; 1.

DR	pfam; PF00560; LRR; 2.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	SMART; SM00013; LRRNT; 1.
DR	PROSITE; PS00237; G-PROTEIN-RECEP-F1_1; 1.
DR	PROSITE; PS50262; G-PROTEIN-RECEP-F1_2; 1.
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW	Phosphorylation; Repeat; Leucine-rich repeat.
FT	SIGNAL 1 17
FT	CHAIN 18 693
FT	DOMAIN 18 366
FT	TRANSMEM 367 387
FT	DOMAIN 388 398
FT	TRANSMEM 399 421
FT	DOMAIN 422 443
FT	TRANSMEM 444 465
FT	DOMAIN 466 485
FT	TRANSMEM 486 508
FT	DOMAIN 509 528
FT	TRANSMEM 529 550
FT	DOMAIN 551 573
FT	TRANSMEM 574 597
FT	DOMAIN 598 608
FT	TRANSMEM 609 630
FT	DOMAIN 631 693
FT	REPEAT 45 68
FT	REPEAT 69 93
FT	REPEAT 95 118
FT	REPEAT 119 143
FT	REPEAT 168 192
FT	REPEAT 193 216
FT	REPEAT 218 240
FT	DISULFID 442 517
FT	CARBOHYD 47 47
FT	CARBOHYD 191 191
FT	CARBOHYD 199 199
FT	CARBOHYD 268 268
FT	CONFLICT 4 4
FT	CONFLICT 88 88
FT	CONFLICT 140 140
FT	CONFLICT 174 174
FT	CONFLICT 191 191
FT	CONFLICT 329 329
SO	SEQUENCE 693 AA; 78697 MW; 46F98699635A1BEC CRC64;
QY	Query Match
QY	Best Local Similarity 4.6%; Score 109; DB 1; Length 693;
Matches	100; Conservative 17.2%; Pred: No: 0.87; Gaps 21;
QY	18 LPNG-INGIKDARKVTVG----VIGSGDFAKSLTIRLIRCGYHVVIGSRNPFASEFFF 71
Db	61 IPKGATGLHDLEKIEISQNDALEITEGNVFSSL-----PKL----- 97
QY	72 HWDVTHEDALTKTNTIIFVAIHRERYTLSWLRLHLIVG-----KILI 114
Db	98 -----HEIRTEKANKL-MKIDQDAFHQLPSRLYLLISNTGLSFLPVTHKVSFOKL 149
QY	115 DVSNMRINQYPPESNAEYLASLFPDSLIVKGFFNVSAWALQLGPKDASRQVVICSNNTQA 174
Db	150 DVQDNIIHIRTIERNTFMGLSS---ESVILR-----LNKNGIQE 184
QY	175 RQQVIELAROLNPIPIDLGSSLSSAREIENPLRLPTLWRGPVVAISLATEFFLYSFVRD 234
Db	185 IKD----HAFFNGTCLDELNLSDNYNLEKLPPEKVFGQAGIPVVLIDISRTRISFLPSHGLE 239
QY	235 VIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGL----- 275
Db	240 PIKKLRARSTYKLLKLP--DVNKFRSLIEANFTYPSSHCCAFTRKTQNTEFYPICSMSPA 297
QY	276 -----LAAYQOLYXGTKY---RRF-----PWLETWLQCR 302
Db	298 KQDLGEQTGKRKHRRSAEVDYISHYGTREFGVENEFDYGLCNEWVDFVCSPSKPDAFNPC 357
QY	303 KQLG-----LLSFFFAMVHVA-----YSLLCLPMRRSERVLFNMYQQWHAN 344
Db	358 DIMGYNVRLVLIWFINILAITGNTTIVLILSSQYKLTVP---REMONTLAFAD--- 4CC
QY	345 TENSWNEEVRIEMYISFGIMSLGLSLAVTSIPSVSNALNRE-----FSFIQ 399
Db	409 -----LCIGIVLLEIASVDIOTKSRYVNAIDWQTGAGCNAAGFFTVFA 455
QY	396 STIGYVALLISTPH-----VLIYGWKRAF----- 41
Db	453 SELSVYTITLITERWHTITYAMQLNRKVRIRHAVIIMVFGWMAFTVALIPIFGISSYM 511
QY	420 -----EEYYKRYTPPNFVLALVLPSSIVILDLLQLCRY 452
Db	513 KVSICLPMHETPFSQAYV--IFLLVNLVLAFTVCIYCIVCY 553
RESULT 7	
ID	FRE6 YEAST
ID	FRE6 YEAST STANDARD; PRT; 712 AA.
AC	Q12473;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Ferric reductase transmembrane component 6 precursor (EC 1.16.1.7)
DE	(Ferric-chelate reductase 6).
GN	FRE6 OR YLI051C OR L0593.
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX	NCBI_TaxID=4932;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=S288C / AB972;
RC	MEDLINE=97313267; PubMed=9169871;
RA	Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA	Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA	Entian K.-D., Floeth M., Goffeau A., Hebling U., Neumann K.,
RA	Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA	Louis E.-J., Messenguy F., Mewes H.-W., Miessga T., Moestl D.,
RA	Mueler-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA	Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA	Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA	Underwood A.P., Urrestarazu L.A., Vandembol M., Verhasselt P.,
RA	Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RT	"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.", Nature 387:87-90 (1997).
RL	-
CC	-!- CATALYTIC ACTIVITY: NADH + 2 Fe (3+) = NAD (+) + 2 Fe (2+).
CC	-!- COFACTOR: FAD (Probable).
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC	-!- SIMILARITY: Belongs to the FRE / CYBB family.
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CC	EMBL; 247973; CAA88006.1; -.
DR	EMBL; 273156; CAA97503.1; -.
DR	PIR; S50969; S50969.
DR	GermanLine; 142046; -.
DR	SGD; S0003974; FRE6.
DR	Interpro; IPR002916; Ferric reductase.
DR	pfam; PF01794; Ferric_reduct; 1.
KW	Oxidoreductase; Electron transport; Transmembrane; Iron transport;
KW	FAD; NAD; Glycoprotein; Signal; Multigene family.
FT	SIGNAL 1 17 POTENTIAL.
FT	CHAIN 18 712 FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 6 FAD (POTENTIAL).
FT	NP_BIND 493 499

FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 288 308 POTENTIAL.
 FT TRANSMEM 329 349 POTENTIAL.
 FT TRANSMEM 361 381 POTENTIAL.
 FT TRANSMEM 388 408 POTENTIAL.
 FT TRANSMEM 417 437 POTENTIAL.
 FT TRANSMEM 478 498 POTENTIAL.
 FT TRANSMEM 550 570 POTENTIAL.
 FT DOMAIN 553 556 POLY-LEU.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 655 655 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 712 AA; 81989 MW; 5224F12B5154BAA CRC64;

Query Match 4.6%; Score 109; DB 1; Length 712;
 Best Local Similarity 18.8%; Pred. No. 0.9; Mismatches 51; Indels 142; Gaps 17;
 Matches 72; Conservative 51; Mismatches 119; Indels 142; Gaps 17;

Qy 88 IIFVIAHREHYHTSL---WDLRHLVGKILIDVSNNMRINQYPPESNAEYLASL 136
 Db 183 IIAVFFHMHSYHNGINRALFAASRFVNVTIRGHFVLPFLWD---KHANHFKFLNVEVFGL 238
 Qy 137 FPDSTLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDIGLS 196
 Db 239 MPNSL-----EAW----- 246
 Qy 197 SAREIENLPLRLFTIMRGPVVVVAISIATFFL-YSFVRDVTHPYARNQOSDFYKIPIEV 255
 Db 247 -----IIFGYTLANIIFLSISYIIDPYNLIFNSHLSQFTRL--LA 284
 Qy 256 NKTLPIAVAITLISLYLAGLLAAAYQLYGTYKRRFPWPLETWLQCRQKOLIGLMSFFAMV 315
 Db 285 DRS-GILAFQTPLIIFTARNSPLEFLTGVKFNSP-----ISPHKWMGRIMVNATI 336
 Qy 316 H-VAYSTCLCPMRSERVYLEFLNMAVQOVHANTENSWNNEEEVRIEMYISFGIMSGLNL 374
 Db 337 HSLSYSL-----FAIINHAK-----ISNK-----QLIWKFGIASITVLCVL 373
 Qy 375 AVTSIPSNSNALNWRREFSFIQSTLGYVALLI---STFHMLIY-GWKRAFE-----EE 422
 Db 374 LVLSLIGIVRK---RHYEFFLYTHITLALLFFYCCWQHVVKIFNGWKEIWIVSLINGLEK 429
 Qy 423 YYRFYTPPNFVIALVLPSPIVLDL 446
 Db 430 LFRIWN---IIQFRFPKATLNL 449

RESULT 8
 FRE7_YEAST STANDARD; PRT; 629 AA.
 ID AC Q12333;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ferric reductase transmembrane component 7 (EC 1.16.1.7) (Ferric-chelate reductase 7).
 DE FRE7 OR YOL152W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=96132030; PubMed=8553699;
 RA Casamayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,
 RA Lafuente M.J., Gancedo C., Arino J.;
 RT "DNA sequence analysis of a 13 kbp fragment of the left arm of yeast
 chromosome XV containing seven new open reading frames.";
 RT Yeast 11:1281-1288(1995);
 RL

RESULT 9
 FSHR_HUMAN STANDARD; PRT; 695 AA.
 ID FSHR_HUMAN P23945; Q16225;
 AC P23945; Q16225;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 DE receptor).
 GN FSHR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CC -!- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
 CC -!- COFACTOR: FAD (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the FRE / CYBB family.
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 or send an email to license@isb-sib.ch).
 CC EMBL; 248239; CAA88276.1; -.
 DR EMBL; Z74894; CAA99174.1; -.
 DR PIR; S60385; S60385.
 DR GermOnline; 143574; -.
 DR SGD; S0005512; FRE7.
 DR Interpro; IPR002916; Ferric_reduct.
 DR Pf01794; Ferric_reduct_1.
 DR Oxidoreductase; Electron_transport; Transmembrane; Iron_transport;
 KW FAD; NAD; Glycoprotein; Multigene_family.
 NP BIND 369 375 FAD (POTENTIAL).
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 108 128 POTENTIAL.
 FT TRANSMEM 168 188 POTENTIAL.
 FT TRANSMEM 195 215 POTENTIAL.
 FT TRANSMEM 238 258 POTENTIAL.
 FT TRANSMEM 266 286 POTENTIAL.
 FT TRANSMEM 293 313 POTENTIAL.
 FT TRANSMEM 422 442 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 541 541 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 629 AA; 71996 MW; 2384480E9289C16F CRC64;

Query Match 4.6%; Score 107.5; DB 1; Length 629;
 Best Local Similarity 21.7%; Pred. No. 1; Mismatches 77; Indels 83; Gaps 17;
 Matches 57; Conservative 46; Mismatches 77; Indels 83; Gaps 17;

Qy 214 GPVVAISLATTEFLYFSFVRDVTHPYARNQOSDFYKIPIEVNKTLPIAVAITLISLY-L 272
 Db 123 GTFLVVMATTLYLIVCFVP--HPFYR-PCAGFGSPPLSV--RAGIMAISLVPPVFL 175
 Qy 273 AG-----LLAAAYQLYGTYKRRFPWPLETWLQCRQKOLIGLMSFFAMVHVAYSLCLPM 325
 Db 176 SGKINVIGWLVLGSLYE----KINTYHQW-----ASILCLFFPSWVH----IPF 215
 Qy 326 RRSERVYLEFLNMAVQOVHANTENSWNNEEEVRIEMYISFGIMSGLNL 380
 Db 216 LROARH---EGGYERMH---QRWKASDMWR----SGVPPLFLNLWLSSLIPIARRH 262
 Qy 381 --SYNSNALNWRREFSFIQSTLGYVALLISTFHV-----LIYGKRAFEEEYR- 425
 Db 263 FYETFLQHW---ILANGFYISLR---YHVYPELNISHMVLVATIVWW--FAQLFYRL 311
 Qy 426 ---FYTPPNFVIALVLPSPIVL 444
 Db 312 AVKGYLRPGRSFMASTIANVSIV 334

OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A., AND VARIANTS ALA-307 AND SER-680.
 RP TISSUE=Ovary;
 RC MEDLINE=91222171; PubMed=1709010;
 RA Minegishi T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.;
 RT "Cloning and sequencing of human FSH receptor cDNA.";
 RL Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
 RN [2] SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=93246012; PubMed=1301382;
 RX Kelton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.D.;
 RA Rosenthal J.L., Overton S.A., Wands G.D., Kuzeja J.B., Luchette C.A.,
 RA Chappel S.C.;
 RT "The cloning of the human follicle-stimulating hormone receptor and
 its expression in COS-7, CHO, and Y-1 cells.";
 RL Mol. Cell. Endocrinol. 89:141-151(1992).
 RN [3] SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=93075197; PubMed=1359889;
 RX Gromoll J., Gudermann T., Nieschlag E.;
 RA "Molecular cloning of a truncated isoform of the human follicle-
 stimulating hormone receptor.";
 RT Biochem. Biophys. Res. Commun. 188:1077-1083(1992).
 RN [5] SEQUENCE OF 1-342 FROM N.A.
 RP TISSUE=Testis;
 RX MEDLINE=95011044; PubMed=7926278;
 RA Gromoll J., Dankbar B., Gudermann T.;
 RT "Characterization of the 5' flanking region of the human follicle-
 stimulating hormone receptor gene.";
 RL Mol. Cell. Endocrinol. 102:93-102(1994).
 RN [6] SEQUENCE OF 286-695 FROM N.A., AND VARIANT SER-680.
 RP MEDLINE=95000244; PubMed=7916967;
 RX Gromoll J., Ried T., Holtgreve-Grez H., Nieschlag E., Gudermann T.;
 RA "Localization of the human FSH receptor to chromosome 2p21 using a
 genomic probe comprising exon 10.";
 RT J. Mol. Endocrinol. 12:265-271(1994).
 RN [7] 3D-STRUCTURE MODELING OF 49-228.
 RP MEDLINE=96363672; PubMed=8747461;
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,
 RA Hendrickson W.A., el Tayar N.;
 RT "Structural predictions for the ligand-binding region of glycoprotein
 hormone receptors and the nature of hormone-receptor interactions.";
 RL Structure 3:1341-1353 (1995).
 RN [8] VARIANTS ALA-307; ARG-524 AND SER-680.
 RP MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshultz R., Dailey G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes.";
 RL Nat. Genet. 22:231-238 (1999).
 RN [9] ERRATUM.
 RP Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshultz R., Dailey G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373 (1999).
 RN [10] VARIANTS ALA-307 AND SER-680.
 RP MEDLINE=22054685; PubMed=12059813;

RA Asatiani K., Gromoll J., Eckardstein S.V., Zitzmann M., Nieschlag E.,
 RA Simoni M.;
 RT "Distribution and function of FSH receptor genetic variants in normal
 men.";
 RT Andrologia 34:172-176 (2002).
 RL [11] VARIANT OHSS IIE-449;
 RX MEDLINE=22812036; PubMed=12930927;
 RA Vasseur C., Rodien P., Beau I., Desroches A., Gerard C., Matthieu E.,
 RA de Poncheville L., Chaplot S., Savagner F., Croue A.,
 RA Lahlon N., Descamps P., Misrahi M.;
 RT "A chorionic gonadotropin-sensitive mutation in the
 follicle-stimulating hormone receptor as a cause of familial
 gestational spontaneous ovarian hyperstimulation syndrome.";
 RL New Engl. J. Med. 349:753-759 (2003).
 RN [12] VARIANT OHSS ASN-567;
 RX MEDLINE=22812037; PubMed=12930928;
 RA Smits G., Olatunbosun O., Delbaere A., Pierson R., Vassart G.,
 RA Costagliola S.;
 RT "Ovarian hyperstimulation syndrome due to a mutation in the
 follicle-stimulating hormone receptor.";
 RL New Engl. J. Med. 349:760-766 (2003).
 CC -!- FUNCTION: Receptor for follicle-stimulating hormone. The activity
 of this receptor is mediated by G proteins which activate
 adenylylate cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Short;
 CC IsoId=P23945-1; Sequence=Displayed;
 CC
 CC -!- TISSUE SPECIFICITY: Sertoli cells and ovarian granulosa cells.
 CC -!- DISEASE: Defects in FSHR are a cause of ovarian hyperstimulation
 syndrome (OHSS) [MIM:608115]. OHSS is a disorder which occurs
 either spontaneously or most often as an iatrogenic complication
 of ovarian stimulation treatments for in vitro fertilization. The
 clinical manifestations vary from abdominal distention and
 discomfort to potentially life-threatening, massive ovarian
 enlargement and capillary leak with fluid sequestration.
 CC Pathologic features of this syndrome include the presence of
 multiple serous and hemorrhagic follicular cysts lined by
 luteinized cells, a condition called hyperreactio luteinalis.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC FSH/LSH/TSH subfamily.
 CC -!- SIMILARITY: Contains 5 leucine-rich (LRR) repeats.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M65085; AAA52477.1; --.
 DR EMBL; S59900; AAB26480.1; --.
 DR EMBL; M95489; AAA52478.1; --.
 DR EMBL; X68044; CAA48179.1; --.
 DR EMBL; S73199; AAB32071.1; --.
 DR EMBL; S73526; AAB32225.1; --.
 DR PIR; 157661; ORHUFF.
 DR PDB; 1XUN; 15-MAY-97.
 DR Genew; HGNC:3969; FSHR.
 DR MIM; 136435; --.
 DR MIM; 608115; --.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:004963; F:follicle stimulating hormone receptor activity; TAS.
 DR GO; GO:0007292; P:female gamete generation; TAS.
 DR GO; GO:0008585; P:female gonad development; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.

FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 367 387 1 (POTENTIAL).
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 399 421 2 (POTENTIAL).
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 444 465 3 (POTENTIAL).
 FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 486 508 4 (POTENTIAL).
 FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 529 550 5 (POTENTIAL).
 FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 574 597 6 (POTENTIAL).
 FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 630 7 (POTENTIAL).
 FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 64 68 LRR 1.
 FT REPEAT 69 93 LRR 2.
 FT REPEAT 119 143 LRR 3.
 FT REPEAT 170 192 LRR 4.
 FT REPEAT 193 216 LRR 5.
 FT REPEAT 218 240 LRR 6.
 FT DISULFID 442 517 BY SIMILARITY.
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFFLICT 293 293 S -> A (IN REF. 1).
 FT CONFFLICT 2 2 T -> S (IN REF. 1).
 FT CONFFLICT 13 13 V -> A (IN REF. 1).
 FT CONFFLICT 60 60 V -> M (IN REF. 1).
 FT CONFFLICT 166 166 Q -> H (IN REF. 1).
 FT CONFFLICT 215 215 K -> R (IN REF. 1).
 FT CONFFLICT 247 247 S -> T (IN REF. 1).
 FT CONFFLICT 334 334 D -> N (IN REF. 1).
 FT CONFFLICT 349 349 E -> K (IN REF. 1).
 FT CONFFLICT 352 352 T -> A (IN REF. 1).
 FT CONFFLICT 383 383 V -> E (IN REF. 1).
 FT CONFFLICT 407 407 A -> T (IN REF. 1).
 FT CONFFLICT 421 421 V -> I (IN REF. 1).
 FT CONFFLICT 427 427 T -> S (IN REF. 1).
 FT CONFFLICT 435 435 D -> N (IN REF. 1).
 FT CONFFLICT 483 483 L -> V (IN REF. 1).
 FT CONFFLICT 550 550 T -> I (IN REF. 1).
 FT CONFFLICT 586 586 A -> V (IN REF. 1).
 FT CONFFLICT 607 607 S -> L (IN REF. 1).
 FT CONFFLICT 691 691 R -> H (IN REF. 1).
 SQ SEQUENCE 695 AA; 78172 MW; E9EBEDB29C79C450 CRC64;

Query Match Best Local Similarity 4.4%; Score 104.5; DB 1; Length 695; Matches 91; Conservative 91; Mismatches 169; Indels 199; Gaps 21; Gaps 21; Qy 18 LPNG-INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVGSRNPKFASEFFPHVVDV 66 Db 61 IPKGAFSGFGDLEKI-----EISQNDVLEVIEAN---VFSNLPKL-----97 Qy 77 THEDALTTKNIIFVAIREHRTSLWDLRHLVGC-----KILIDVSN 119 Db 98 --HEIRIEKANNL-IYIDPDAFQNLPNRLYLISNTGVTKHLPAVKHQIQLQKVLDIQN 154 Qy 120 MRINQYPESSNAEYLASFPSLFDSSLLVKGFTVVSAWALQLGPKDASRQVYICSNNIQARQQVI 179 Db 155 INIH-----TVERNSFVGLSFESMLWL---SKNGIREIHNC-----189 Qy 180 ELARQLNRPIDLGSSSAREIENPLRLFTLWRGPVUVASLATPFPLSFVIRDVHPI 239 Db 190 ----FNGTQOLDELNLNSDNDNLLELPNDVFQGASGPVILLDISRTRHSYQJENKL 244 Qy 240 ARNQOSDFYKIP----IEIVNKTL-----PIVAILL-----267 Db 245 RAKSTYNLKLUPLSLEKFTVTIMEASLTYPSPHCCAPANTRQISDLHPICNKSLRQEVDVM 304

Oy 268 ----SIVYLAGLLAAAYQLYYGTKYRFF----PPWLETWLOCRKQLG--- 306 Db 305 TOARGQRVSLAEDGESELLAKERDTMSEPDYDLCNEVVDVICSPPEPDTFNPCEDEMHD 364 Oy 307 --LISFFFAMVHVA-----YSICLPMRRSERYLFINMAYQVHANIENSWE 351 Db 365 LRVLIWFISILAITGNNTIVLVLITSOYKLTVP----RFLMCNLAFAD 364 Oy 352 EEVWRIEMYISFGIMSLIGLISLAVTSIPSVSNALNRE-----FSFIQSTIG-- 399 Db 409 -----LCLGIGIYLLIASVDINTKQVHNIAIDWQTGAGCDAAGFPTVFASELSVIT 459 Oy 400 YVALLISTFH-----VLIYGKRAFEEEYRYFTPPNFV-LALVLP 439 Db 460 LTAITLERWHITTHAMOLOCKVQLRHAASIMLVGWIAFTVALPPIRGISSYMKVSCILP 519 Oy 440 SIVILDILQL 449 Db 520 MDIDSQL 529

RESULT 11
 SOTB_ECO57 ID SOTB_ECO57 STANDARD; PRT; 396 AA.
 AC P58529;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Sugar efflux transporter.
 GN SOTB OR Z2173 OR ECS2135.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 RN NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsuka E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RA "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 RT DNA Res. 8:11-22 (2001).
 RL -- FUNCTION: Involved in the efflux of sugars. The physiological role may be the reduction of the intracellular concentration of toxic sugars or sugar metabolites. Transports L-arabinose and to a lesser extent IPTG. Seems to contribute to the control of the arabinose regulon (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Probable).
 CC -!- SIMILARITY: Belongs to major facilitator superfamily. SotB (TC 2.A.1.2) family.
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OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

NCBI_TAXID=562;

DR PIR; H85721; H85721..1.

DR PAMAP; MP_00517; -; 1.

DR InterPro; IPR007114; MPS.

DR EMBL; AP002557; BAB35558..1; -.

DR Pfam; PF00083; sugar_tr_1..

PROSITE; PS50850; MFS; 1..

KW Transport; Sugar transport; Transmembrane; Complete proteome.

FT TRANSMEM 15 35 POTENTIAL.

FT TRANSMEM 50 70 POTENTIAL.

FT TRANSMEM 81 101 POTENTIAL.

FT TRANSMEM 103 123 POTENTIAL.

FT TRANSMEM 136 156 POTENTIAL.

FT TRANSMEM 170 190 POTENTIAL.

FT TRANSMEM 209 229 POTENTIAL.

FT TRANSMEM 246 266 POTENTIAL.

FT TRANSMEM 275 295 POTENTIAL.

FT TRANSMEM 299 319 POTENTIAL.

FT TRANSMEM 333 353 POTENTIAL.

FT TRANSMEM 364 384 POTENTIAL.

SQ SEQUENCE 396 AA; 42568 MW; CB6A209B0BE6D4F0 CRC64;

Query Match 4.4%; Score 104; DB 1; Length 396;

Best Local Similarity 18.8%; Pred. No. 1;

Matches 85; Conservative 72; Mismatches 148; Indels 146; Gaps 20;

QY 31 VTVGVIGSGDFRAKSLTIRLIRCGYHVWVIGSRNPKFASEPPPHVVDVTHEDALTKTNNIF 90 MEDLINE=97251357; PubMed=9097039;

Db 31 VPVGILL--SDIAQSFHMQTAQVGIMILTIYAWVVALMSLPFMLMWSQVERRKILICLFWVF 88

QY 91 VAIHREHYTSWLIDLRLHLLVGKILIDVSNMRINQYPESSNAEYLASLFPSLIVKGFNWVS 150

Db 89 IASHVLSFLS-WSFTVLVISR-----GVAFAHAIF-----WSITA 123

QY 151 AWALQLGP--KDASRQVYICSNNIQRQQVIELAR-----QINIFIPIDLGSL---- 195

Db 124 SLAIRMAPAGKRAQALSILATGTAAWVIGLPLGRIVGQYFGWRMTFFAIGIGALITLLC 183

QY 196 -----SSAREIENPLRLFTIWRGPVVAISLAT-----FFFLYSFVRDVHRY 239

Db 184 LTKLPLLPSEHSGSLKSLPL---LFRPAIMSIVLTWVWVTAHYTASY---IEPF 235

QY 240 ARN---QOSDFYKIPIEIWNKTLPIAVITLSSLVYLAGLLAAAYQOLYYGTYKRRFPFWLE 296

Db 236 VQNIAGFSANF-----ATALLLGGAGIIGSVTFGKLGNOYAS---- 274

QY 297 TWLQCRKQCLGLSFFFAMHVAYSCLPMRRSERYLFLNMAYQQHANIENSNEEVNR 356

Db 275 -----ALVNSTAIALLVLCLALLPAANSE-----IHLGVLSIF----WG 309

QY 357 IEMYISFGIMSLGLSL-----LAVTSIPSVSN-----ALNMRFSFIOST 397

Db 310 IAMMITIGLGMQVKVTLALAPDATDVAMALFSGIFNIGGACALVGNQSVLHNS---MSM 364

QY 398 LGYVALLISTFHVLIYG-----WKRAFEE 422

Db 365 IGYVG-TVPAAFLIWSIIIFRRWPVILEQ 394

RESULT 12

SOTB_ECOLI STANDARD; PRT; 396 AA.

ID_SOTB_ECOLI STANDARD; PRT; 396 AA.

AC P31122; P76883; P77353; 01-JUL-1993 (Rel. 26, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Sugar efflux transporter.

SOTB OR B1528.

DR STRAIN=K12 / MG1655;

DR MEDLINE=97426617; PubMed=9278503;

DR Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12." Science 277:1453-1474 (1997). [2]

DR RN SEQUENCE FROM N.A.

DR RC STRAIN=K12;

DR RX MEDLINE=97251357; PubMed=9097039;

RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampai G., Seki Y., Sivasundaram S., Tagami H., Takeda J., RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map." DNA Res. 3:363-377(1996). [3]

RN RP SEQUENCE OF 217-396 FROM N.A.

RX MEDLINE=93186717; PubMed=8383113;

RA Cohen S.P., Haechler R., Levy S.B.; "Genetic and functional analysis of the multiple antibiotic resistance (mar) locus in Escherichia coli." J. Bacteriol. 175:1484-1492(1993). [4]

RN RP CHARACTERIZATION.

RC STRAIN=SBO;

RC MEDLINE=99194728; PubMed=10094697;

RA Bost S., Silva F., Belin D.; "Transcriptional activation of ydeA, which encodes a member of the major facilitator superfamily, interferes with arabinose accumulation and induction of the Escherichia coli arabinose PBAD promoter."; J. Bacteriol. 181:2185-2191(1999). [5]

RC RP STRAIN=JS219;

RC MEDLINE=99369894; PubMed=10438792;

RA Carole S., Pichoff S., Bouche J.-P., "Escherichia coli gene ydeA encodes a major facilitator pump which exports L-arabinose and isopropyl-beta-D-thiogalactopyranoside."; J. Bacteriol. 181:5123-5125(1999).

CC -!- FUNCTION: Involved in the efflux of sugars. The physiological role may be the reduction of the intracellular concentration of toxic sugars or sugar metabolites. Transports L-arabinose and to a lesser extent IPTG. Seems to contribute to the control of the arabinose regulon.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (Probable).

CC -!- SIMILARITY: Belongs to major facilitator superfamily. SotB (TC 2.A.1.2) family.

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CC DR EMBL; AE000250; AAC74601..1; -.

CC DR EMBL; D90795; BAA15210..1; -.

CC DR EMBL; D90796; BAA15218..1; -.

CC DR EMBL; D90797; BAA15230..1; -.

DR EMBL; M96235; -; NOT_ANNOTATED_CDS.
 DR PIR; C64907; C64907.
 DR EcoGene; EG11636; sotB.
 DR HAMAP; MF_00517; -; 1.
 DR InterPro; IPR007114; MFS.
 DR Prosite; PROSITE; PF00083; sugar_tr_-1.
 DR PROSITE; PS50850; MFS; 1.
 KW Transport; Sugar transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 15 35 POTENTIAL.
 FT TRANSMEM 50 70 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 136 156 POTENTIAL.
 FT TRANSMEM 170 190 POTENTIAL.
 FT TRANSMEM 209 229 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 275 295 POTENTIAL.
 FT TRANSMEM 299 319 POTENTIAL.
 FT TRANSMEM 333 353 POTENTIAL.
 FT TRANSMEM 364 384 POTENTIAL.
 SEQUENCE 396 AA; 42538 MW; CB6A34CA4EE6D4F0 CRC64;

Query Match 4.4%; Score 104; DB 1; Length 396;
 Best Local Similarity 18.8%; Pred. No. 1;
 Matches 85; Conservative 72; Mismatches 148; Indels 146; Gaps 20;

QY 31 VTVGVIGSGDFAKSLITRLRGCGYHVGSRNPKEASEFFPHWVWDVTHEDALTQTNIF 90
 31 VPVGGLL--SDIAQSFFMOTAQVGIMLTIVAWVALMSLPLFMLMTSQVERRKLLICLFLVVF 88

QY 91 VAIHREHYTSLWDLRHLIYGKILLIDVSNNMRINQYEPESNAEYLASLFDPLSLIVKGFMWS 150
 89 IASHVLISFLS-WSFTLVISR-----GVAFAHALF-----WSITA 123

QY 151 AWALQIGP--KDASRQVYICSNNIQARQQVIELAR-----QLNFTIPIDLGLS----- 195
 124 SLAIRMAPAGKRAQALSLIATGTLAMVIGLPIGRIVGQYFGWRMFTFAIGIGALITLIC 183

QY 196 -----SSAREEENLPLRIFTLWRGPVVAISLAT-----FFFLYSFVRDVHYPY 239
 184 LIKLPLPSEHSGSLSIPL---FRRPAMSIYLLTVVVTAHYASY----IEPF 235

QY 240 ARN--QOSDFYKIPILEIWNKTLPIAVITLISLVLAGLLAAVQLYIYGTKYRFPPWLE 296
 236 VONIAGFSANF-----ATALLLIGGAGIIGSVIFGKGKGNQYAS----- 274

Db 297 TWLQCRKQOGLLSFFFAMVHVAVSLCLPMRMRSERVLFLNMAVQVTHANTENSNEEEWR 356
 275 -----ALVSTAIALLVCALLLPAANSE-----IHIGVLSIFF-----WG 309

QY 357 IEMYVISFGIMSLGLISL-----LAVTSIPSVD-----ALNWREFSFIOST 397
 310 IAMMIIGLGMQVKVLAAPDATDVAMALFSGIFNIGIGAGALVGQNQVSLHWS----MSM 364

QY 398 LGYVALLISTEHVLIYGG-----WKRAFEE 422
 365 IGYVG-AVPAFAALIWSIIIIFRRWPVTEEQ 394

RESULT 13
 NPT1_MOUSE STANDARD; PRT; 465 AA.

ID NPT1_MOUSE
 AC Q61983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Renal sodium-dependent phosphate transport protein 1 (sodium/phosphate cotransporter 1) (Na⁽⁺⁾/Pi cotransporter 1) (Renal sodium-phosphate cotransporter 1) (Renal Na⁽⁺⁾-dependent phosphate cotransporter 1).
 DE transport protein 1 (Renal Na⁽⁺⁾-dependent phosphate cotransporter 1).
 DE SLC17A1 OR NPT1.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC
 RX MEDLINE=95335846; PubMed=7611445;
 RA Chong S.S., Kozak C.A., Liu L., Kristjansson K., Dunn S.T., Bourdeau J.E., Hughes M.R.;
 RA "Cloning, genetic mapping, and expression analysis of a mouse renal sodium-dependent phosphate cotransporter."
 RT Am. J. Physiol. 268:F1038-F1045(1995).
 RL -!
 CC FUNCTION: Important for the resorption of phosphate by the kidney.
 CC May be involved in actively transporting phosphate into cells via Na⁽⁺⁾ cotransport in the renal brush border membrane.
 CC -!
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!
 CC TISSUE SPECIFICITY: Kidney.
 CC -!
 CC SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
 CC
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 CC
 CC
 DR EMBL; X77241; CRA54459.1; -.
 DR PIR; S69915; S69915.
 DR MGI; MGI:103209; SIC17a1.
 DR InterPro; IPR007114; MFS.
 DR Prosite; PS50850; MFS; 1.
 DR TIGRFAMS; TIGR00894; 2A0114eu; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Transport; Symport; Sodium transport; Transmembrane; Glycoprotein.
 FT TRANSMEM 79 99 POTENTIAL.
 FT TRANSMEM 117 137 POTENTIAL.
 FT TRANSMEM 176 196 POTENTIAL.
 FT TRANSMEM 199 219 POTENTIAL.
 FT TRANSMEM 260 280 POTENTIAL.
 FT TRANSMEM 304 324 POTENTIAL.
 FT TRANSMEM 337 356 POTENTIAL.
 FT TRANSMEM 363 383 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT TRANSMEM 429 449 POTENTIAL.
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 465 AA; 51589 MW; C67E25A2C291EEF CRC64;

Query Match 4.4%; Score 103; DB 1; Length 465;
 Best Local Similarity 18.7%; Pred. No. 1.5;
 Matches 76; Conservative 64; Mismatches 142; Indels 124; Gaps 16;

QY 110 GKKLIDVSNNMRINQYEPESNAEYLASLFDPLSLIVKGFMVVAWALQLGPKDA---SROVY 166
 Db 79 GLISSLSSVTFGMVWVQAP--VGYLISGTYPMKRIGSSLFLSLSLIPAAQVGALVI 135

QY 167 ICSNNIQARQQVIELARQNLFI----FDLGSISAREIENLPLRIFTLWRGPVVV---- 218
 Db 136 VCRVHQGIAQGTVSTGQHEIWVKWAPPLERGRITS----WTLGFM--GPFIVLVS 187
 QY 219 -----AISLATFFFLYFSFVRDVHYPYARNQODF----- 247
 Db 188 GFICDLGLGWMFVYIGIVGCVLISLNSWFLFFDDPKD--HPYMSSEKDYIISLMMQDAS 245
 QY 248 --YKIPIBIWNKTLPIAVITLIS----- 268
 Db 246 SGROSPLRIKAMIKSLPWLAILNSFAIWNSLIVVTPTFISTVHLVNRENGILSSLP 305
 QY 269 -LVYLAGLILAAAYQLYYGGTKYRFPPWLETWLQCRKQOLGLLSFFFAVMVAVSCLPMR 326

Db	306 YLLAVICGILAGQMSDFLIRK-----ISSIVTVRKLFTTLGSCFCPVIFTMCILLYLSVN 359	
Qy	327 RSERYLFLNMAYQQVHANIENSWNEEVWRI----YISF--GIMSL---GLLSLLAV 376	
Db	360 FYSTVIFLTAA---NSTLSFSYCCGQLINALDIAPRYGYELKAVTALIGMGGGLISTLA 415	
Qy	377 TSIRPSVSNALNREFSFTQSTLGYVALLISTFHLI---IYGKRR 417	
Db	416 GLINQDPEYAWKISFLMAGINTVCLV--FYFLFAKGEIQDWAK 458	
RESULT 14		
ID NUCC_NEPOL	STANDARD; PRT; 391 AA.	
AC Q9TKV6;		
DT 10-OCT-2003	(Rel. 42, Created)	
DT 10-OCT-2003	(Rel. 42, Last sequence update)	
DT 10-OCT-2003	(Rel. 42, Last annotation update)	
DE NAD(P)H-quinone oxidoreductase chain H, chloroplast (EC 1.6.5.-)		
DE (NAD(P)H dehydrogenase, chain H) (NADH-plastoquinone oxidoreductase 49 kDa subunit).		
DE NDHH.		
GN Nephroselmis olivacea.		
OG Chloroplast.		
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;		
OC Chlorodendrales; Chlorodendraceae; Nephroselmis.		
OX NCBI_TAXID=31312;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=NIES-484;		
RX MEDLINE=99398694; PubMed=10468594;		
RA Turmel M., Otis C., Lemieux C.;		
RT "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast genomes.";		
RT PROC. Natl. Acad. Sci. U.S.A. 96:10248-10253 (1999).		
RL CC	-!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE PLASTOQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF	
CC CC	-!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P) (+) + plastoquinol.	
CC CC	-!- SIMILARITY: Belongs to the complex I 49 kDa subunit family.	
CC CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC CC	EMBL; AF137379; AAD54891.1; -.	
CC CC	DR InterPro; IPR001135; Oxidored_49kDa.	
CC CC	DR Pfam; PF00346; complex1_49Kd; 1.	
CC CC	DR PROSITE; PS00535; COMPLEX1_49K; 1.	
KW CC	Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.	
SQ SEQUENCE 391 AA; 44913 MW; 9A40AEC6B995B25E CRC64;		
Query Match	4.4%; Score 102.5; DB 1; Length 391;	
Best Local Similarity	17.9%; Pred. No. 1.3;	
Matches	80; Conservative 70; Mismatches 124; Indels 173; Gaps 20;	
Qy	85 KTNIIIFVIAHREHYTLSWDLRHLV---GKLID-----VSNMMRINQYPE 127	
Db	5 KTDPMIVSM-GPHHPMSMGVLVLTLDGENVLDCEPVVGYLHRGMKTAENRTIVQYLP 63	
Qy	128 --SNAEYLASLFPDSLIVKGFMNVSAWALQIGPKDASRQVYICSNNIQAROOVIELARQL 185	
Db	64 YVTRWDYLAATMTEAITV-----NAPERLANIEVPRRA 96	
Qy	186 NFPIPDGLSISAREIENLPIRLFTLWRGPVVAISLATEFFLYSFVRDVHYPARNQOS 245	
RESULT 15		
ID Y304_BRUME	STANDARD; PRT; 220 AA.	
AC Q8YD73;		
DT 28-FEB-2003	(Rel. 41, Created)	
DT 28-FEB-2003	(Rel. 41, Last sequence update)	
DT 28-FEB-2003	(Rel. 41, Last annotation update)	
DE Hypothetical protein BMEII0304.		
GN BMEII0304.		
OS Brucella melitensis.		
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
OC Brucellaceae; Brucella.		
OX NCBI_TAXID=29459;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=16M / ATCC 23456 / Biotype 1;		
RX MEDLINE=20020109; PubMed=11756688;		
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski I., Larsen N., D'Souza M., Bernal A., Mazur M., Gotsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrides N., Overbeek R.;		
RA RT	"The genome sequence of the facultative intracellular pathogen Brucella melitensis."	
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).		
CC CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential). -!- SIMILARITY: Belongs to the UPF0191 family.	
CC CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC CC	EMBL; AE009669; AAL53546.1; -.	
DR DR	PIR; AG3547; AG3547.	
DR DR	HAMAP; MF_01207; -; 1.	
DR DR	InterPro; IPR007916; UPF0191.	
PFam; PF05252; UPF0191; 1.		
KW Hypothetical protein; Transmembrane; Complete proteome.		
FT TRANSMEM	20 39 POTENTIAL.	
FT TRANSMEM	54 72 POTENTIAL.	
FT TRANSMEM	85 104 POTENTIAL.	
FT TRANSMEM	124 146 POTENTIAL.	
FT TRANSMEM	153 175 POTENTIAL.	
FT TRANSMEM	179 198 POTENTIAL.	
SQ SEQUENCE 220 AA; 24815 MW; 182C0244743B17PA CRC64;		

Query Match 4.3%; Score 102; DB 1; Length 220;
Best Local Similarity 23.8%; Pred. No. 0.72;
Matches 43; Conservative 25; Mismatches 51; Indels 62; Gaps 7;

Search completed: March 1, 2004, 23:31:14
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 1, 2004, 23:34:47 ; Search time 63 Seconds
(without alignments)
1521.644 Million cell updates/sec

Title: US-09-455-486-6
Perfect score: 2351
Sequence: 1 MESISMGSPIKSLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454
Scoring table: BIOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 809742
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

- 1: Published Applications AA:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_E_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_E_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% No.	Score	Query Match Length	DB ID	Description

Result	% No.	Score	Query Match Length	DB ID	Description

RESULT 1
US-09-888-257A-10
; Sequence 10, Application US/09888257A
; Publication No. US20030060612A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Polakis, Paul
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin

NO

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF TUMOR
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: P5002R1
CURRENT APPLICATION NUMBER: US/09/888, 257A
PRIOR APPLICATION NUMBER: US 60/063, 540 ✓
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: US 60/089, 653 ✓
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 60/099, 792 ✓
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/103, 678 ✓
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: US 60/235, 451 ✓
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/08439

ALIGNMENTS

16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284
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not near.

Sequence 10, Appl
Sequence 34, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 162, App
Sequence 37654, A
Sequence 15, Appl
Sequence 1, Appl
Sequence 50, Appl
Sequence 51, Appl
Sequence 879, App
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Sequence 11, Appl
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Sequence 37, Appl
Sequence 714, App
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Sequence 313, App
Sequence 123, App
Sequence 39, Appl
Sequence 80, Appl

PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-888-257A-10

Query Match 100.0%; Score 2351; DB 10; Length 454;
Best Local Similarity 100.0%; Pred. No. 8e-222; Mismatches 0; Indels 0; Gaps 0;
Matches 454; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

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Db 1 MESISMGMGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGRGVWVIGS 60
Qy 61 RNPKEASEEFFPHVVDVTHEDALTTKTNIIFVAIREHYTSIWLDRHLVGKILLDVSNM 120
Db 61 RNPKEASEEFFPHVVDVTHEDALTTKTNIIFVAIREHYTSIWLDRHLVGKILLDVSNM 120
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Db 181 LARQLNFIPIDLGSISSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVIPHYA 240
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Db 301 CRKQQLGLLSFFFAMVHAYSLCLPMRMRSERVLFLNMAQOQVHANIENSWNEEVRIEMY 360
Qy 361 ISFGIMSLGLLAVTSIPSVSNALNWRFSFIOSTLGVALLISTFHVLIGWKRAFE 420
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Qy 421 EYYYRFYTPPNFVLALVLPSIVILDILQLCRYPD 454
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RESULT 2
US-10-165-044-8
; Sequence 8, Application US/10165044
; Publication No. US20030149531A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016-02
; CURRENT APPLICATION NUMBER: US/10-165, 044
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087, 520
; PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: US 60/091, 183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323, 873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455, 486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SEQ ID NO 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-165-044-8

Query Match 100.0%; Score 2351; DB 14; Length 454;
Best Local Similarity 100.0%; Pred. No. 8e-222; Mismatches 0; Indels 0; Gaps 0;
Matches 454; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

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Db 301 CRKQQLGLLSFFFAMVHAYSLCLPMRMRSERVLFLNMAQOQVHANIENSWNEEVRIEMY 360
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Db 361 ISFGIMSLGLLAVTSIPSVSNALNWRFSFIOSTLGVALLISTFHVLIGWKRAFE 420
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Db 421 EYYYRFYTPPNFVLALVLPSIVILDILQLCRYPD 454

RESULT 3
US-10-239-607-29
; Sequence 29, Application US/10239607
; Publication No. US20030219761A1
; GENERAL INFORMATION:
; APPLICANT: Saatcioglu, Fahri
; TITLE OF INVENTION: NO. US20030219761A1el Prostate-Specific or
; TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, and
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
; FILE REFERENCE: 50218/003002
; CURRENT APPLICATION NUMBER: US/10/239, 607
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09410
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191, 929
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 29
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-239-607-29

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Best Local Similarity 100.0%; Pred. No. 8e-222; Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPDKDASRQVYICSNNTIQRQQVIE 180

Db 181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240
181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240

QY 241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300
241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300

Db 301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360
301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360

QY 361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
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Db 421 EYYRFYTPPNFVLAVALVLPISIVLDLQLCRYPD 454
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QY 121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPDKDASRQVYICSNNTIQRQQVIE 180
121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPDKDASRQVYICSNNTIQRQQVIE 180

Db 181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240
181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240

QY 241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300
241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300

Db 301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360
301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360

QY 361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420

Db 421 EYYRFYTPPNFVLAVALVLPISIVLDLQLCRYPD 454
421 EYYRFYTPPNFVLAVALVLPISIVLDLQLCRYPD 454

RESULT 4

US-10-295-027-574

; Sequence 574, Application US/10295027
; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Sequence 574, Application US/10295027
; Publication No. US20030232350A1

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 574
LENGTH: 454

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-295-027-574

Query Match

100.0%; Score 2351; DB 15; Length 454;

Best Local Similarity 100.0%; Pred. No. 8e-222; Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVVIGSGDFAKSLTIRLIRCGYHVVIGS 60
1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVVIGSGDFAKSLTIRLIRCGYHVVIGS 60

QY 61 RNPKEASEEFFPHVVDVTTHEDALTKTNIIFVATHREHTSYLWDLRHLVKGKILIDVSNNM 120
61 RNPKEASEEFFPHVVDVTTHEDALTKTNIIFVATHREHTSYLWDLRHLVKGKILIDVSNNM 120

QY 121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPDKDASRQVYICSNNTIQRQQVIE 180
121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALOLGPDKDASRQVYICSNNTIQRQQVIE 180

Db 181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240
181 LARQNFIPIDGLSLSAREIENPLRLFTLWRGPVVAISLATFFFLYSFVRDVHPYA 240

QY 241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300
241 RNQOSDFYKIPIEVNKTLPVATLSSLVLAGLLAAVOLYYGTYKRRFPWPLETWQ 300

Db 301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360
301 CRKQOLGLISFFFAMVHVAYSLCPLPMRRSERYLFNMAVQVHANIENSNEEEVRIEMY 360

QY 361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
361 ISFGIMSLGLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420

Db 421 EYYRFYTPPNFVLAVALVLPISIVLDLQLCRYPD 454
421 EYYRFYTPPNFVLAVALVLPISIVLDLQLCRYPD 454

RESULT 5

US-10-392-190-2

; Sequence 2, Application US/10392190
; Publication No. US20040005598A1

; GENERAL INFORMATION:

; APPLICANT: Devaux, Bridgitte
; APPLICANT: Eberhard, David
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillian, Kenneth J.
; APPLICANT: Wattanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel G.

; TITLE OF INVENTION: PUMPCn COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: P2994R1C1-US

CURRENT APPLICATION NUMBER: US/10/392,190
; CURRENT FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: US 60/235,451
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: PCT/US01/30290
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-392-190-2

Query Match 100.0%; Score 2351; DB 15; Length 454;

Best Local Similarity 100.0%; Pred. No. 8e-222; Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHVG 60
; 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHVG 60
Db 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
; 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120

QY 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
; 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
Db 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180
; 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180

QY 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180
; 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180
Db 181 LARQLNFIPIIDGLSISSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA 240
; 181 LARQLNFIPIIDGLSISSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA 240

QY 181 LARQLNFIPIIDGLSISSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA 240
; 181 LARQLNFIPIIDGLSISSSAREIENLPLRLFTLWRGPVVAISLATFFFLYSFVRDVHRYA 240
Db 241 RNQOSDFYKIPIEIUNKLPIAVITLISLVLAGLLAAVOLYYGKRRPPWLETWLO 300
; 241 RNQOSDFYKIPIEIUNKLPIAVITLISLVLAGLLAAVOLYYGKRRPPWLETWLO 300

QY 301 CRKQQLGLLSFFFAMVHVAYSLCLPMRSERYLFNMAQQVHANIENSNEEBVRIEMY 360
; 301 CRKQQLGLLSFFFAMVHVAYSLCLPMRSERYLFNMAQQVHANIENSNEEBVRIEMY 360
Db 360 301 CRKQQLGLLSFFFAMVHVAYSLCLPMRSERYLFNMAQQVHANIENSNEEBVRIEMY 360
; 360 301 CRKQQLGLLSFFFAMVHVAYSLCLPMRSERYLFNMAQQVHANIENSNEEBVRIEMY 360

QY 361 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAFE 420
; 361 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAFE 420
Db 420 361 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAFE 420
; 420 361 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAFE 420

QY 421 EBYVRFYTPPNFVLALVLPSIVILDILQLCRYPD 454
; 421 EBYVRFYTPPNFVLALVLPSIVILDILQLCRYPD 454
Db 454 421 EBYVRFYTPPNFVLALVLPSIVILDILQLCRYPD 454
; 454 421 EBYVRFYTPPNFVLALVLPSIVILDILQLCRYPD 454

RESULT 7

US-09-802-520-1

; Sequence 1, Application US/09802520

; Publication No. US20020187472A1

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Faris, Mary

; APPLICANT: Chen, Huei-Mei

; APPLICANT: Ison, Craig H.

; TITLE OF INVENTION: STEAP-RELATED PROTEIN

; FILE REFERENCE: PC-0037 US

; CURRENT APPLICATION NUMBER: US/09/802,520

; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PERL program

; SEQ ID NO 1

; LENGTH: 490

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20020187472A1 7492448CD1

US-09-802-520-1

Query Match 97.6%; Score 2294; DB 9; Length 490;
; Best Local Similarity 100.0%; Pred. No. 3.5e-216; Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHVG 60
; 1 MESISMGMSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHVG 60
Db 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
; 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120

QY 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
; 61 RNPKFASEFPHPVVDVTHEDALTAKTNIIFVAIHEREHYSILWDLRHLVKGKILDVSNNM 120
Db 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180
; 121 RINQYPESNAEYLASLFPDSLIVKGFFNTVSAWALQLGPKDASRQVYICSNNIQARQVIE 180

QY 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 Db 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 QY 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 Db 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 QY 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 Db 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 ;
 RESULT 8
 US-10-239-607-14
 ; Sequence 14, Application US/10239607
 ; Publication No. US20030219761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saatcioglu, Fahri
 ; TITLE OF INVENTION: NO. US20030219761A1el Prostate-Specific or
 ; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
 ; FILE REFERENCE: 50218/003002
 ; CURRENT APPLICATION NUMBER: US/10/239, 607
 ; PRIOR APPLICATION NUMBER: PCT/US01/09410
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 32
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-239-607-32
 Query Match 97.4%; Score 2290; DB 15; Length 490;
 Best Local Similarity 99.8%; Pred. No. 8.7e-216; Indels 0; Gaps 0;
 Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHWIGS 60
 Db 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHWIGS 60
 QY 61 RNPKFASEFPHVVDVTHEDALTKTNTIFVAIHRHEYTSWLDRHLLVGKILIDSNNM 120
 Db 61 RNPKFASEFPHVVDVTHEDALTKTNTIFVAIHRHEYTSWLDRHLLVGKILIDSNNM 120
 QY 121 RINOYPESNAEYLASLPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQO VIE 180
 Db 121 RINOYPESNAEYLASLPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQO VIE 180
 QY 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 Db 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 QY 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 Db 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 QY 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 Db 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 ;
 RESULT 9
 US-10-239-607-32
 ; Sequence 32, Application US/10239607
 ; Publication No. US20030219761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saatcioglu, Fahri
 ; TITLE OF INVENTION: NO. US20030219761A1el Prostate-Specific or
 ; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
 ; FILE REFERENCE: 50218/003002
 ; CURRENT APPLICATION NUMBER: US/10/239, 607
 ; PRIOR APPLICATION NUMBER: PCT/US01/09410
 ; PRIOR FILING DATE: 2001-03-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 32
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-239-607-32
 Query Match 86.6%; Score 2036; DB 15; Length 419;
 Best Local Similarity 99.7%; Pred. No. 5.7e-191; Indels 0; Gaps 0;
 Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHWIGS 60
 Db 1 MESISMGGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHWIGS 60
 QY 61 RNPKFASEFPHVVDVTHEDALTKTNTIFVAIHRHEYTSWLDRHLLVGKILIDSNNM 120
 Db 61 RNPKFASEFPHVVDVTHEDALTKTNTIFVAIHRHEYTSWLDRHLLVGKILIDSNNM 120
 QY 121 RINOYPESNAEYLASLPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQO VIE 180
 Db 121 RINOYPESNAEYLASLPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQO VIE 180
 QY 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 Db 181 LAROLNFIPIIDLGSLSAREIENPLRFLTILWRGPVVVAISLATFFFLYSFVRDVH PYA 240
 QY 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 Db 241 RNQOSDFYKIPIEIVNKTLPIAVATLSSLVLAGLLAAAYQLYYGTKRFPFWRGPVVAISLATFFFLYSFVRDVH PYA 300
 QY 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 Db 301 CRKQQLGLLSFFFAMVHVAISLCLPMRMRSERYLFLNMAAYQVHANIENSWNEEVWRIEMY 360
 ;
 RESULT 10
 US-10-182-951-6
 ; Sequence 6, Application US/10182951
 ; Publication No. US20030138895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.

Query Match 54.1%; Score 1272; DB 14; Length 488;
 Best Local Similarity 54.5%; Pred. No. 6.4e-116; Mismatches 108; Indels 12; Gaps 4;
 Matches 242; Conservative 82; Mismatches 108; Indels 12; Gaps 4;

Qy 3 SISMMGSPKSLSETCLPNCINGIKDARKTVGVIGSGDFAKSLTIRLRCGYHVVIGSRN 62
 Db 11 SLHLVDSSSLAK--VPD----EAPK--VGLGSGDFARSLATRLVGSGFKVWVGSRN 60

Qy 63 PKFASEFFPHVVDVTHEDALTKTNIFVAIHCHEHTSLLWDLRHLLVGKILIDVSN--NM 120
 Db 61 PKRTARLPSAAQVTFQEEAVSSPEVIFVAVFREHYSSLCSLSLDQLAGKILVDSNPTEQ 120

Qy 121 RINQYPPESNAEYLASLIPDSLIVKGFPNVSAWALQLGPKDASROVYICSNNIQARQVIE 180
 Db 121 EHLQHRESNAEYLASLIPPTCTVVKAFNVISAWTLQAGPRDGNRQVPICGDQEPEAKRAVE 180

Qy 181 LARQNFIPIDGLSISAREIENPLRIFTWWRGPVVAISLATEFFLYSFVRDVHRYA 240
 Db 181 MALAMGFMPVDMGSLASAWEVEMPLRLLPAWKVPTLLALGLFVCFYAVNFVDRDQPYV 240

Qy 241 RNQQSDFYKIPIBIVNKTLPIAVITLISLVLAGLLAAAYQLYGTYKRRFPFWLETWLO 300
 Db 241 QESQNKKFKLPSVNTTLPCVAVVLLVLPGVLAALQRLRGRTKYQRFPDWLDHNLQ 300

Qy 301 CRKQIGLILSFFPAMHVAYSLCLPMRMRSERVLFLNMAQQHANTENSWNNEEEVWRIMEY 360
 Db 301 HRKOIGLILSFFPACALHALYSFCLPLRAHYDLVNLANKSHLWEEEVWRIMEY 360

Qy 361 ISRGIMSLGLLISLLAVTSIPSNSNALNWRFSFIQSTLGIVALLISTFHVLIGWRAFE 420
 Db 361 LSLGVLAIGTLLSLLAVTSLPSIANSLNWRFSFVQSSLGFVALVLISTHTLTGWTAFE 420

Qy 421 EYYRFYTPPNFVLAIVLPSIVL 444
 Db 421 ESRYKEYLPPPTFTLILVPCVIL 444

RESULT 11
 US-09-747-835A-13
 ; Sequence 13, Application US/09747835A
 ; Patent No. US20020146692A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua

Query Match 54.0%; Score 1269; DB 9; Length 488;
 Best Local Similarity 54.3%; Pred. No. 1.3e-115; Mismatches 108; Indels 12; Gaps 4;
 Matches 241; Conservative 83; Mismatches 108; Indels 12; Gaps 4;

Qy 3 SISMMGSPKSLSETCLPNCINGIKDARKTVGVIGSGDFAKSLTIRLRCGYHVVIGSRN 62
 Db 11 SLHLVDSSSLAK--VPD----EAPK--VGLGSGDFARSLATRLVGSGFKVWVGSRN 60

Qy 63 PKFASEFFPHVVDVTHEDALTKTNIFVAIHCHEHTSLLWDLRHLLVGKILIDVSN--NM 120
 Db 61 PKRTARLPSAAQVTFQEEAVSSPEVIFVAVFREHYSSLCSLSLDQLAGKILVDSNPTEQ 120

Qy 121 RINQYPPESNAEYLASLIPDSLIVKGFPNVSAWALQLGPKDASROVYICSNNIQARQVIE 180
 Db 121 EHLQHRESNAEYLASLIPPTCTVVKAFNVISAWTLQAGPRDGNRQVPICGDQEPEAKRAVE 180

Qy 181 LARQNFIPIDGLSISAREIENPLRIFTWWRGPVVAISLATEFFLYSFVRDVHRYA 240
 Db 181 MALAMGFMPVDMGSLASAWEVEMPLRLLPAWKVPTLLALGLFVCFYAVNFVDRDQPYV 240

Qy 241 RNQQSDFYKIPIBIVNKTLPIAVITLISLVLAGLLAAAYQLYGTYKRRFPFWLETWLO 300
 Db 241 QESQNKKFKLPSVNTTLPCVAVVLLVLPGVLAALQRLRGRTKYQRFPDWLDHNLQ 300

Qy 301 CRKQIGLILSFFPAMHVAYSLCLPMRMRSERVLFLNMAQQHANTENSWNNEEEVWRIMEY 360
 Db 301 HRKOIGLILSFFPACALHALYSFCLPLRAHYDLVNLANKSHLWEEEVWRIMEY 360

Qy 361 ISRGIMSLGLLISLLAVTSIPSNSNALNWRFSFIQSTLGIVALLISTFHVLIGWRAFE 420
 Db 361 LSLGVLAIGTLLSLLAVTSLPSIANSLNWRFSFVQSSLGFVALVLISTHTLTGWTAFE 420

Qy 421 EYYRFYTPPNFVLAIVLPSIVL 444
 Db 421 ESRYKEYLPPPTFTLILVPCVIL 444

RESULT 12
 US-10-239-607-36
 ; Sequence 36, Application US/10239607
 ; Publication No. US20030219761A1
 ; GENERAL INFORMATION:

; APPLICANT: Saatcioglu, Fahri
; TITLE OF INVENTION: No. US20030219761A1 Prostate-Specific or
; TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, and
; FILE REFERENCE: 50218/003002
; CURRENT APPLICATION NUMBER: US/10/239, 607
; CURRENT FILING DATE: 2002-09-24
; PRIORITY NUMBER: PCT/US01/09410
; PRIORITY FILING DATE: 2001-03-23
; SEQ ID NO 36
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-239-607-36

Query Match 54.0%; Score 1269; DB 15; Length 488;
Best Local Similarity 54.3%; Pred. No. 1.3e-115; Matches 241; Conservative 83; Mismatches 108; Indels 12; Gaps 4; Db

QY 3 SISMMGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHVVIGSRN 62
11 SLHLVDSDSLAK--VPD----EAPK--VGILGSGDFARSIASTRLVGSGFKVVGSRN 60

QY 63 PKFASEFPHPVVDVTHEDALTKTNTIFVAIHRHYTSWLDRHLIVKGKLLIDVSN--NM 120
61 PKRTARLYPSAAQVTFOBEAVSSPEVIFVAVFREHYSSLCISLSQLAGKILNDVSNPTEQ 120

QY 121 RINOYPESNAEYLASFPLDSLIVKGENVVSAWALQIGPKDASRQVYICSNNIQARQVIE 180
121 EHLQHRESNAEYLASFPLCTVKAENVISAWTLQAGPRDGNRQVPICGDQEAKRAVE 180

QY 181 LARQLNFIPIDGLSLSARTEINLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
181 MALAMGFMPVDMGLSLASAWEVEAMPRLLPWKVPTILALGLFVCFYAVNFVRDVLPYV 240

QY 241 RNQQSDFYKIPTEIVNKTLPIVATLILSVLAGLAAAYQLYGGTKYRFPPLLETWLO 300
241 QESQNKKFFKLPVSVVNTTLPCVAVVLISLVLPGVTLALQLRRGTQYORFPDWLDHWLQ 300

QY 301 CRKQQLGILSFFAMVHVAYSLCIPMRSERYLFLINMAYQOQHANIENSWNEEVWRIEMY 360
301 HRKQIGLISFFCAALHALYSFCIPLRRAHYDLVNLAVKQLANKSHLWEEVWRMEIY 360

QY 361 ISFGIMSIGLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLTYGWKRAFE 420
361 LSLGVLAIGTISLLAVTSLPSIANSLNWREFSFVQSSLGFVALVLTSLHTLTGYWTRADE 420

QY 421 EYYRFYTPPNFVLALVLPSIVIL 444
421 ESRYKFYLPPTFTLILVPCVIL 444

Db

QY RESULT 13
US-10-239-607-38

; Sequence 38, Application US/10239607
; Publication No. US20030219761A1

; GENERAL INFORMATION:

; APPLICANT: Saatcioglu, Fahri
; TITLE OF INVENTION: No. US20030219761A1 Prostate-Specific or
; TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, and
; TITLE OF INVENTION: Diagnostic and Therapeutic Methods
; FILE REFERENCE: 50218/003002
; CURRENT APPLICATION NUMBER: US/10/239, 607
; CURRENT FILING DATE: 2002-09-24
; PRIORITY NUMBER: PCT/US01/09410
; PRIORITY FILING DATE: 2001-03-23
; PRIORITY APPLICATION NUMBER: US 60/191, 929
; PRIORITY FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-239-607-38

Query Match 54.0%; Score 1269; DB 15; Length 488;
Best Local Similarity 54.3%; Pred. No. 1.3e-115; Matches 241; Conservative 83; Mismatches 108; Indels 12; Gaps 4; Db

QY 3 SISMMGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLRCGYHVVIGSRN 62
11 SLHLVDSDSLAK--VPD----EAPK--VGILGSGDFARSIASTRLVGSGFKVVGSRN 60

QY 63 PKFASEFPHPVVDVTHEDALTKTNTIFVAIHRHYTSWLDRHLIVKGKLLIDVSN--NM 120
61 PKRTARLYPSAAQVTFOBEAVSSPEVIFVAVFREHYSSLCISLSQLAGKILNDVSNPTEQ 120

QY 121 RINOYPESNAEYLASFPLDSLIVKGENVVSAWALQIGPKDASRQVYICSNNIQARQVIE 180
121 EHLQHRESNAEYLASFPLCTVKAENVISAWTLQAGPRDGNRQVPICGDQEAKRAVE 180

QY 181 LARQLNFIPIDGLSLSARTEINLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVHRYA 240
181 MALAMGFMPVDMGLSLASAWEVEAMPRLLPWKVPTILALGLFVCFYAVNFVRDVLPYV 240

QY 241 RNQQSDFYKIPTEIVNKTLPIVATLILSVLAGLAAAYQLYGGTKYRFPPLLETWLO 300
241 QESQNKKFFKLPVSVVNTTLPCVAVVLISLVLPGVTLALQLRRGTQYORFPDWLDHWLQ 300

QY 301 CRKQQLGILSFFAMVHVAYSLCIPMRSERYLFLINMAYQOQHANIENSWNEEVWRIEMY 360
301 HRKQIGLISFFCAALHALYSFCIPLRRAHYDLVNLAVKQLANKSHLWEEVWRMEIY 360

QY 361 ISFGIMSIGLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLTYGWKRAFE 420
361 LSLGVLAIGTISLLAVTSLPSIANSLNWREFSFVQSSLGFVALVLTSLHTLTGYWTRADE 420

QY 421 EYYRFYTPPNFVLALVLPSIVIL 444
421 ESRYKFYLPPTFTLILVPCVIL 444

Db

QY RESULT 14
US-09-965-529-21

; Sequence 21, Application US/09965529
; Publication No. US20020182671A1

; GENERAL INFORMATION:

; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Duyng Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731 USA

; CURRENT APPLICATION NUMBER: US/09/965, 529

; CURRENT FILING DATE: 2001-09-26
; PRIORITY NUMBER: 60/149, 641; 60/164, 203; PCT/US00/22315
; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020182671A1 1859305CD1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 1, 2004, 19:57:15 ; Search time 83 Seconds

(without alignments)

1725.847 Million cell updates/sec

Title: US-09-455-486-6

Perfect score: 2351

Sequence: 1 MESISMGSPLSETCLPN.....ALVLPSIVILDLLQLCRYPD 454

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_ratodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score % Query Match Length DB ID Description

1 2290 97.4 490 4 Q8IUE7 Q8iue7 homo sapien

2 2284 97.2 490 4 Q8NFT2 Q8nft2 homo sapien

3 2239.5 95.3 489 11 Q8BWB6 Q8bw6 mus musculu

4 1318 56.1 488 11 Q8C5F0 Q8c5f0 mus musculu

5 1316 56.0 488 11 Q99P41 Q99p41 rattus norv

6 1316 56.0 488 11 Q8CI59 Q8ci59 mus musculu

7 1316 56.0 526 11 Q80ZF3 Q80zf3 mus musculu

8 1306 55.6 514 11 Q924Z1 Q924z1 mus musculu

9 1272 54.1 488 4 Q86SP6 Q86sp6 homo sapien

10 1272 54.1 498 4 Q7Z389 Q7z389 homo sapien

11 1269 54.0 488 4 Q9NTB5 Q9ntb5 homo sapien

12 1252.5 53.3 487 4 Q8NEW6 Q8new6 homo sapien

13 1245.5 53.0 487 4 Q8TF03 Q8tf03 homo sapien

14 1074.5 45.7 456 4 Q8TDP3 Q8tdp3 homo sapien

15 1064.5 45.3 470 11 Q923B6 Q923b6 mus musculu

16 1057.5 45.0 470 11 Q91W31 Q91w31 mus musculu

ALIGNMENTS

RESULT 1

ID	Q8IUE7	PRELIMINARY;	PRT;	490 AA.
AC	Q8IUE7;			
DT	01-MAR-2003	(TREMBLrel. 23, Created)		
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	STAMP1.			
OS	Homo sapiens (Human).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
[1]				

SEQUENCE FROM N.A.

TISSUE=prostate;

MEDLINE=22229309; PubMed=12095985;

Korkmaz K.S., Elbi C.C., Korkmaz C.G., Loda M., Hager G.L., Saatcioglu F., "Molecular cloning and characterization of STAMP1, a highly prostate specific six-trans-membrane protein that is overexpressed in prostate cancer.", J. Biol. Chem. 277:36689-36696 (2002).

EMBL; AY008445; AAG32149.1; -

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR004455; NADPoxred_F420.

DR Pfam; PF03807; F420_oxidored; T.

DR SEQUENCE 490 AA; 56027 MW; D1971A84880F7E51 CRC64;

Query Match 97.4%; Score 2290; DB 4; Length 490; Best Local Similarity 99.8%; Pred. No. 4.1e-176; Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0; O91ze8 mus musculu Q7tp88 ratmus norv Q9g150 bus scrofa Q924zz mus musculu Q9cwr7 mus musculu Q924j9 mus musculu Q9h5r1 homo sapien Q8wrb0 homo sapien Q9h7y1 homo sapien Q8nius corynebacte Q8xgs2 ralstonia s Q82ax0 streptomyce Q930k7 rhizobium m Q8yk44 anabaena sp Q9kr6 streptomyce Q8gfg4 rhodococcus Q9bc62 rhizobium l Q8gfg3 rhodococcus Q8tyq9 methanopyru Q82q14 archaeoglob 029059 archaeoglob Q9f418 mycobacteri Q83vc1 streptomyce Q9jn78 streptomyce Q8gfg1 rhodococcus

QY 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
Db 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
QY 181 LARQINFIPIDIGLSLSARETENPLRLFTLWRGPVVVAISLATFFFLYSFVRDVH PYA 240
Db 181 LARQINFIPIDIGLSLSARETENPLRLFTLWRGPVVVAISLATFFFLYSFVRDVH PYA 240
QY 241 RNQOSDFYKIPIEVNKTLPPIAVITLSSLVLAGLLAAAYOLYYGTYKRRFPWPLETWLO 300
Db 241 RNQOSDFYKIPIEVNKTLPPIAVITLSSLVLAGLLAAAYOLYYGTYKRRFPWPLETWLO 300
QY 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360
Db 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360
QY 361 ISFGIMSLGLSLLAVTSIPSVSNALNREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
Db 361 ISFGIMSLGLSLLAVTSIPSVSNALNREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
QY 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360
Db 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360
QY 421 EYVRFYTPPNFVLALVLP SIVL 444
Db 421 EYVRFYTPPNFVLALVLP SIVL 444
Db 361 ISFGIMSLGLSLLAVTSIPSVSNALNREFSFIQSTLGYVALLISTFHVLIGWKRAFE 420
QY 421 EYVRFYTPPNFVLALVLP SIVL 444
Db 421 EYVRFYTPPNFVLALVLP SIVL 444

RESULT 2

Q8NFT2 PRELIMINARY; PRT; 490 AA.
AC Q8NFT2;
DT 01-OCT-2002 (TREMBrel. 22, Created)
DT 01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)
DE Six-transmembrane epithelial antigen of prostate 2.
GN STEAP2.
OS Homo sapiens (Human)
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Parkka K.P., Helenius M.A., Visakorpi T.;
RA "Cloning and characterization of a novel six-transmembrane protein
STEAP2, down-regulated in androgen-independent prostate cancer.";
RA Submitted (DBC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP455138; AACN04080.1; -.
DR Genew; HGNC:17885; STEAP2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004455; NADPoxred_F420.
DR Pfam; PF03807; F420_oxidored; I.
DR Transmembrane.
SQ SEQUENCE 490 AA; 55961 MW; F2E9C30CDCACEF81 CRC64;

Query Match 97.2%; Score 2284; DB 4; Length 490;
Best Local Similarity 99.8%; Pred. No. 1.2e-175;
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESISMGMSPKSLSETCLPNGINGIKDARKTVGVIGSGDFAKSLTIRLIRCGYHWVG 60
Db 1 MESISMGMSPKSLSETCLPNGINGIKDARKTVGVIGSGDFAKSLTIRLIRCGYHWVG 60
QY 61 RNPKEASEFPFHVDVTHEDALT KTNII FVAIRHEHTSLWDLRHLVKGKILIDVSNNM 120
Db 61 RNPKEASEFPFHVDVTHEDALT KTNII FVAIRHEHTSLWDLRHLVKGKILIDVSNNM 120
QY 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
Db 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
QY 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
Db 121 RINOYPESNAEYLASIFPDLSLIVKGFNVVSAWALQLGPKDASROVYICSNNTIARQOQIE 180
QY 181 LARQINFIPIDIGLSLSARETENPLRLFTLWRGPVVVAISLATFFFLYSFVRDVH PYA 240
Db 180 LARQINFIPIDIGLSLSARETENPLRLFTLWRGPVVVAISLATFFFLYSFVRDVH PYA 240
QY 241 RNQOSDFYKIPIEVNKTLPPIAVITLSSLVLAGLLAAAYOLYYGTYKRRFPWPLETWLO 300
Db 240 RNQOSDFYKIPIEVNKTLPPIAVITLSSLVLAGLLAAAYOLYYGTYKRRFPWPLETWLO 300
QY 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360
Db 301 CRKQIGLISFFFAMVHVAVSLCILPMPMRSERYLFLNMAYQVHANTENSWNEEEVWRIEMY 360

Db	300 CRKQQLGLLISPFVAVVHVAWSLCIPLMRRSERYLFLNAYQOQVHANTENAWNEEVRIEMY	QY	424 YRFYTPPNFVLALVLPSIVL 444
Qy	361 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAFE 420	Db	424 YKFYLPPTEFTILLPCVIL 444
Db	360 ISFGIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLITFHVLIGWKRAFA 419	RESULT 5	Q99P41
Qy	421 EYVYRFYTPPNFVLALVLPSIVL 444	ID	Q99P41
Db	420 EYVYRFYTPPNFVLALVLPSIVL 443	AC	Q99P41;
		DT	01-JUN-2001 (TREMBrel. 17, Created)
		DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)
		DE	Tumor suppressor gene.
		OS	Rattus norvegicus (Rat).
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]
		OC	NCBI_TaxID=10090;
		RN	[1]
		RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.	RC	SEQUENCE=Dunning; TISSUE=Prostatic carcinoma; MEDLINE=20424188; PubMed=10969787;
RX	STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=22354683; PubMed=12466851;	RA	Steiner M.S., Zhang X., Wang Y., Lu Y.; "Growth inhibition of prostate cancer by an adenovirus expressing a novel tumor suppressor gene, pHyde.", Cancer Res. 60:4419-4425(2000).
RA	The RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Consortium.	RL	[2]
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).	RP	SEQUENCE FROM N.A.
RL	EMBL; AK078769; BAC37383.1; -.	RA	Lu Y., Rinaldy A.R.; Steiner M.S.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR	MGD; MGI:1915678; Tsap6.	RL	[3]
DR	GO; GO:0006118; P:electron transport; IEA.	DR	Steiner M.S., Rinaldy A.; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR	InterPro; IPR004455; NADPoxred_F420.	DR	EMBL; AF238865; AAI78207.1; -.
DR	Pfam; PF03807; F420_oxidored; 1.	DR	GO; GO:0006118; P:electron transport; IEA.
SQ	SEQUENCE 488 AA; 54780 MW; FDFC4F42AE503D11 CRC64;	DR	InterPro; IPR004455; NADPoxred_F420.
		DR	Pfam; PF03807; F420_oxidored; 1.
		SQ	SEQUENCE 488 AA; 54640 MW; 59FFC07121919FDCA CRC64;
	Query Match 56.1%; Score 1318; DB 11; Length 488; Best Local Similarity 56.2%; Pred. No. 8.4e-98; Matches 248; Conservative 81; Mismatches 100; Indels 12; Gaps 4;		Query Match 56.0%; Score 1316; DB 11; Length 488; Best Local Similarity 56.2%; Pred. No. 1.2e-97; Matches 248; Conservative 81; Mismatches 100; Indels 12; Gaps 4;
Qy	6 MMGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHGHWVGSRNPKF 65	Qy	6 MMGSPKSLSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCQHGHWVGSRNPKF 65
Db	14 LVDSDSLAE--VP-----KEAPK--VGILGSGDFARSLATRLVGGFSVWVGSRNPKR 63	Db	14 LVDSDSLAE--VP-----KEAPK--VGILGSGDFARSLATRLVGGFSVWVGSRNPKR 63
Qy	66 ASEFFPHVVDVTHEDALTKTNIIFVAIHREHYTLWDLRHLLVGKILIDVSNNMRIN-- 123	Qy	66 ASEFFPHVVDVTHEDALTKTNIIFVAIHREHYTLWDLRHLLVGKILIDVSNNMRIN-- 123
Db	64 TAGLFFPSLAQVTFQEEAMSPEVIFVAVFREHYSSLCSLADOLAGKILVDDSNPTEKEHL 123	Db	64 TAGLFFPSLAQVTFQEEAMSPEVIFVAVFREHYSSLCSLADOLAGKILVDDSNPTEKEHL 123
Qy	124 QYPESNAEYLASLFPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQQVIELAR 183	Qy	124 QYPESNAEYLASLFPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQQVIELAR 183
Db	184 QLNFTPIDLGSLSAREIENLPLRFLTLMRGPVVAISLATEFLYSFVRDVHPIYARNQ 243	Qy	124 QYPESNAEYLASLFPDSLIVKGFFNVSAWALQLGPKDASRQVYICSNNIQARQQVIELAR 183
Qy	184 AMGFTPPLDMGSLASAREVEAIPRLLLPSWKVPTLALGLSTOSYAVNFIRDVLQPYIRKD 243	Db	184 AMGFTPPLDMGSLASAREVEAIPRLLLPSWKVPTLALGLSTOSYAVNFIRDVLQPYIRKD 243
Db	244 QSDFYKPIEINKTLPPIVATLISLVLVLAGLAAAYQLYYGTKYRFRPPWLETWLQCRK 303	Qy	244 QSDFYKPIEINKTLPPIVATLISLVLVLAGLAAAYQLYYGTKYRFRPPWLETWLQCRK 303
Qy	244 ENKPYKMPLESVNTTLPVCVAVVLLSLVYLPGVLAALQLRGTQYQRFPDWLDHQLQRK 303	Db	244 ENKPYKMPLESVNTTLPVCVAVVLLSLVYLPGVLAALQLRGTQYQRFPDWLDHQLQRK 303
Qy	304 QLGILSFFAMVHVAYSLCIPMRSERYLFLNAYQVHANTENSWEEVRIEMYSF 363	Qy	304 QLGILSFFAMVHVAYSLCIPMRSERYLFLNAYQVHANTENSWEEVRIEMYSF 363
Db	304 QIGLILSFFFAMHLHALYSFCCLPLRRSHRYDLVNLANKSRLWVEEVWRMEIYSL 363	Db	304 QIGLILSFFFAMHLHALYSFCCLPLRRSHRYDLVNLANKSRLWVEEVWRMEIYSL 363
Qy	364 GIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAPEEEY 423	Qy	364 GIMSLGLLISLLAVTSIPSVSNALNWREFSFIQSTLGVALLISTFHVLIGWKRAPEEEY 423
Db	364 GVLALGMLSLLLAVTSIPSANSLNKEPSFVOSTLGVALMSTMTHTLGWTRAEEHN 423	Db	364 GVLALGMLSLLLAVTSIPSANSLNKEPSFVOSTLGVALMSTMTHTLGWTRAEEHN 423

QY 424 YRFYTPPNFVIALVLP SIVL 444 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
|:|||:|||:|||:|||:|||:|||:
ID Q8C159 PRELIMINARY; PRT; 488 AA. DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
AC Q8C159; DE Tsap6.
DT 01-MAR-2003 (TREMBLrel. 23, Created) OS Mus musculus (Mouse).
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update) OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Similar to RIKEN cDNA 1010001D01 gene. OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GN TSAP6 OR 1010001D01RK. OS NCBI_TaxID=10090;
RN [1]
RN STRAIN=CZECH II;
RA STRAUSBERG R.; RC RT
RL Submitted (SEP-2002) to the EMBL/GenBank/DDJB databases. RP SEQUENCE FROM N.A.
DR EMBL; BC037435; AAH37435.1; -. RX STRAIN=DSMZ ACC331; TISSUE=Bone marrow;
DR MGI; MGI:1915678; Tsap6. RA MEDLINE=22506415; PubMed=12606722;
DR GO: GO:0006118; P:electron transport; IEA. RA Passer B.J., Nancy-Portebois V., Amzallag N., Prieur S., Cans C.,
DR InterPro; IPR004455; NADPoxred_F420. RA Roborel de Climens A., Fiucci G., Bouvard V., Tuynier M., Susini L.,
DR Pfam; PF03807; F420_Oxidored; T. RA Morchoisne S.P., Cribie V., Lespagnol A., Dausset J., Oren M.,
SQ SEQUENCE 488 AA; 54749 MW; 9A08D99C90CF83F4 CRC64; RA Amson R., Telerman A.;
DR "The p53-inducible TSAP6 gene product regulates apoptosis and the cell RT cycle and interacts with Nix and the Myt1 kinase.";
DR PRO: Natl. Acad. Sci. U.S.A. 100:2284-2289(2003). RL EMBL; AY214462; AA038239.1;
DR GO: GO:0006118; P:electron transport; IEA. DR Pfam; PF03807; F420_Oxidored; T.
DR InterPro; IPR004455; NADPoxred_F420. SQ SEQUENCE 526 AA; 58530 MW; 6306CD717B25200A CRC64;

Query Match 56.0%; Score 1316; DB 11; Length 488;
Best Local Similarity 56.2%; Pred. No. 1.2e-97;
Matches 248; Conservative 81; Mismatches 100; Indels 12; Gaps 4;

QY 6 MMGSPKSLSETCLPNGINGIKDARKVTGVGIVGSGDFAKSLTIRLIRCGYHVVIGSRRNPKF DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 14 LVDSGSLAE--VP----KEAPK--VGILGSGDFARSLATRVLVGSFSVVGSRNPKR 63 RX STRAIN=CZECH II;
QY 66 ASEFPFHVVVDVTHEDALT KTNII FVAI HREHTSLWDLRHLUVKGKILIDVSNNMRIN-- DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 64 TAGLFPSLAQVTFQEEAVSSPEVIFVAVFREHYSSLCSLADQLAGKILNDVSNPTEKEHL 123 RA MEDLINE=22506415; PubMed=12606722;
QY 124 QYPESNAEYLASLFPDSLIVKGFFNVSAWALOLGPKDASROWYICSNNTIQAROQVIELAR DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 124 QHRQSNAEYLASLFPACTVVKAFNVI SAWALQAGPRDGNRQVLICSDOPEAKRTISEMAR 183 RA PASSER B.J., NANCY-PORTEBOIS V., AMZALLAG N., PRIEUR S., CANS C.,
QY 184 QLNFIPIDLGSSAREIENPLRLLFTLWRGPVVVAISLATFFFLYSFVRDVHRYARNQ DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:|||:|||:|||:
Db 184 AMGFTTLDMGSLASAREVEAIPLRLLPSWKVPTILLALGLFVCFTYTFNIRDVLQPYIRKD 243 RA MEDLINE=22506415; PubMed=12606722;
QY 244 QSDFYKIPIEVNKTLPPIAVTLLSLVYLAGLLAAAYQLYYGTKYRFRPPWLETWLOCRK DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:|||:|||:
Db 244 ENKEYKMPLSVNTTLPCVAVVLLSLVYLPGVLAALQLRRGTYQRFPDWLHDWLQHRK 303 RA PASSER B.J., NANCY-PORTEBOIS V., AMZALLAG N., PRIEUR S., CANS C.,
QY 304 QLGILSFFFAMVHVAYSICLPMR SERYLFLNMAYQQVHANIENSWEENEVRIEMYISF DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:|||:
Db 304 QLGILSFFFAMVHVAYSICLPMR SERYLFLNMAYQQVHANIENSWEENEVRIEMYISF 363 RA MEDLINE=22506415; PubMed=12606722;
QY 364 GIMSLIGLSSLLAVTSIPS VSNA LN WREFSFPIOSTLGYVALLISTFHVL IYGWKR AFE EEEY DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
|:|||:|||:|||:|||:|||:
Db 364 GVLAGLGMSSLLAVTSIPLRSRSHRDYDLVNLAVKQVLANKSRLWEEEVWRMEIYLSL 363 RA PASSER B.J., NANCY-PORTEBOIS V., AMZALLAG N., PRIEUR S., CANS C.,
QY 424 YRFYTPPNFVIALVLP SIVL 444 RA MEDLINE=22506415; PubMed=12606722;
|:|||:|||:|||:|||:
Db 424 YKFYLPPTFTLILLPCVIL 444 RA PASSER B.J., NANCY-PORTEBOIS V., AMZALLAG N., PRIEUR S., CANS C.,
QY 424 YRFYTPPNFVIALVLP SIVL 444 RA MEDLINE=22506415; PubMed=12606722;
|:|||:|||:|||:
Db 424 YKFYLPPTFTLILLPCVIL 444 RA PASSER B.J., NANCY-PORTEBOIS V., AMZALLAG N., PRIEUR S., CANS C.,
RESULT 7 GN TSAP6 OR 1010001D01RK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
ID Q80ZF3 PRELIMINARY; PRT; 526 AA.
AC Q80ZF3; DE Tsap6.
DT 01-JUN-2003 (TREMBLrel. 24, Created) OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DE Dualin 2. GN TSAP6 OR 1010001D01RK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RESULT 8 Q924Z1 PRELIMINARY; PRT; 514 AA.
ID Q924Z1 AC Q924Z1; DE Dualin 2. DT 01-DEC-2001 (TREMBLrel. 19, Created) OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) RA MEDLINE=22506415; PubMed=12606722;
DE Dualin 2. GN TSAP6 OR 1010001D01RK.

RESULT 9 Q924Z1 PRELIMINARY; PRT; 514 AA.
ID Q924Z1 AC Q924Z1; DE Dualin 2. DT 01-DEC-2001 (TREMBLrel. 19, Created) OC Mammalia; Buttheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) RA MEDLINE=22506415; PubMed=12606722;

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Serru V., Lamblin D., Lenoir C., Manivet P., Vaubourdolle M.,
 RA Kellermann O., Loric S.;
 RT "Molecular cloning and expression of mouse dudulin 2.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY029586; AAK5039.1; -.
 DR MGD; MGI:1915678; Tsap6.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR04455; NADPoxred_F420.
 DR Pfam; PF03807; F420_oxidored; 1.
 SQ SEQUENCE 514 AA; 57268 MW; 339886C288AEC0E2 CRC64;

Query Match 55.6%; Score 1306; DB 11; Length 514;
 Best Local Similarity 56.2%; Pred. No. 8.3e-97; Mismatches 100; Indels 12; Gaps 4;
 Matches 248; Conservative 81; Mismatches 100; Indels 12; Gaps 4;
 QY 6 MMGSPKSLSETCLPNGINGIKDARKTVGVIGSGDFAKSLTIRLIRCYHVVIGSRNPKF 65
 Db 14 IVDSDGSLAB--VP----KEAKP--VGILGSGDFARSLATRLVGGFSWVGSRNPKR 63
 QY 66 ASEFFPHVVDVTHEDALTKNNIFVAIHRHYTSWLDRHLVKGKILIDVSNNMRIN-- 123
 Db 64 TAGLEPLSLAQVTFQEEAVSSPEVIVAVFREHYSSLCISLADQLAGKILVDSNPTEKHL 123
 QY 124 QYPSNAEYLASLFPACTVVKAFNTISAWALQAVPRDGQRQVLICGNDSKAKQRYMEVAR 183
 Db 124 QHRSQNAEYLASLFPACTVVKAFNTISAWALQAVPRDGQRQVLICGNDSKAKQRYMEVAR 183
 QY 184 QINFIPIIDLGSLSASSAREIENLPLRIFTLWRGPVVAISIATFFLYSFVRDVHPIYQ 243
 Db 184 AMGFTPDLDMGLSLASAREVEAIPRLLPSPGKVPTILALGFLFCYTFNFI RDVLOQPYKD 243
 QY 244 QSDFYKIPILEVNKTLPVIAITLISLVLAGLLAAAYQIYGYGTKYRFPFWLETWLGCRK 303
 Db 244 ENKTYKMPPLSVNTTLPVCVAVLISLVLVYLPGVLAALQI RRGTQYQRFDPDWLDHWLQHRK 303
 QY 304 QIGLSSFFFAMRVAYSLCLPMRMRSERYLFLNMAYQOQVHANIENSWNEEWVRIEMY 363
 Db 304 QIGLSSFFFAMVLHALYSFCLPLRRSHYDVLNVLAVKQLANKSRLWVEEEWRMELVLSL 363
 QY 364 GIMSLGLLSSLAVTSI PSVSNALNWREFSFLISTGYVALLISTFHVLIGWKR AFE EYY 423
 Db 364 GVLALGMLSSLAVTSI PSVIANSLNWKEFSFVQSTLGFWVAILSTMVHTLTYGWTRAFEEHN 423
 QY 424 YRFYTPPNFVLAIVLPSIVL 444
 Db 424 YKFYLPPTFTLTLPCVIL 444

RESULT 9
 Q86SF6 ID Q86SF6 PRELIMINARY; PRT; 488 AA.
 AC Q86SF6;
 DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-OCT-2003 (TREMBrel. 24, Last sequence update)
 DE Similar to *duulin*.₂ (TSAP6).
 OS *Homo sapiens* (Human).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBITaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22506415; PubMed=12606722;
 RA Passer B.J., Nancy-Portebois V., Amzallag N., Prieur S., Cans C., Susini L.,
 RA Roborel de Climens A., Fiucci G., Bouvard V., Tuynster M., Susini L.,
 RC TISSUE=Human colon endothelial primary cell culture;
 RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BX538047; CAD97986.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 55593 MW; 69DD23D5A00C2D6B CRC64;

Query Match 54.1%; Score 1272; DB 4; Length 488;
 Best Local Similarity 54.5%; Pred. No. 4.3e-94; Mismatches 82; Indels 12; Gaps 4;
 Matches 242; Conservative 82; Mismatches 108; Indels 12; Gaps 4;
 QY 3 SISMGMGSPKSLSETCLPNGINGIKDARKTVGVIGSGDFAKSLTIRLIRCYHVVIGSRN 62
 Db 11 SLHLDSDSSLAK--VPD----EAKP--VGILGSGDFARSLATRLVGGFSWVGSRN 60
 QY 63 PKFASEFFPHVVDVTHEDALTKNNIFVAIHRHYTSWLDRHLVKGKILIDVSNNMRIN--NM 120
 Db 61 PYRTARLFPSSAAQVTFQEEAVSSPEVIVAVFREHYSSLCISLADQLAGKILVDSNPTEQ 120
 QY 121 RINOYPSNAEYLASLFPACTVVKAFNTISAWALQAVPRDGQRQVLICGNDSKAKQRYMEVAR 180
 Db 121 EHLOHRESNAEYLASLFPACTVVKAFNTISAWALQAVPRDGQRQVLICGNDSKAKQRYMEVAR 180
 QY 181 LARQINFIIDLGSLSASSAREIENLPLRIFTLWRGPVVAISIATFFLYSFVRDVHPIYQ 240
 Db 181 MALAMGFMPPVDMGLSLASAWEVEAMPLRLLPAWKVPTILALGFLFCYTFNFI RDVLOQPYV 240
 QY 241 RNQQSDFYKIPILEVNKTLPVIAITLISLVLAGLLAAAYQIYGYGTKYRFPFWLETWLGCRK 300
 Db 241 QESQNKFKLPPSVWNTTLPVCVAVLISLVLVYLPGVLAALQI RRGTQYQRFDPDWLDHWLQ 300
 QY 301 CRKQGLLSSLAVTSI PSVSNALNWREFSFLISTGYVALLISTFHVLIGWKR AFE EYY 360
 Db 301 HRKOIGLSSFFFAMVLHALYSFCLPLRRSHYDVLNVLAVKQLANKSRLWVEEEWRMELVLSL 360
 QY 361 ISFGIMSLGLLSSLAVTSI PSVSNALNWREFSFLISTGYVALLISTFHVLIGWKR AFE 420
 Db 361 LSLGVLA GTLSLAVTSI PSVIANSLNWKEFSFVQSTLGFWVAILSTMVHTLTYGWTRAFEEHN 420
 QY 421 BEYRFYTPPNFVLAIVLPSIVL 444
 Db 421 ESRVYKFYLPPTFTLTLPCVIL 444

RESULT 10
 Q7Z389 ID Q7Z389 PRELIMINARY; PRT; 498 AA.
 AC Q7Z389;
 DT 01-OCT-2003 (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DE Hypothetical protein DKFZp686H07150.
 GN DKFZp686H07150.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBITaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human colon endothelial primary cell culture;
 RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BX538047; CAD97986.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 55593 MW; 69DD23D5A00C2D6B CRC64;

Query Match	54.1%; Score 1272; DB 4; Length 498;
Best Local Similarity	54.5%; Pred. No. 4.4e-94;
Matches	242; Conservative 82; Mismatches 108; Indels 12; Gaps 4;
Indels	12; Gaps 4;
Qy	3 SISMMGSPKSLSETCLPNGINGIKDARKVTVGIGSGDFAKSLTIRLCGYHVWIGSRN 62
Db	11 SLHLVDSDSSLAK--VPD-----EAPK--VGIIGSGDFARSLATRLVGSGFKVWGSRN 70
Qy	63 PKFASEFFPHVVDVTTHEDALTKTNIIFVAIHRHEHTSLWDLRHLVGKILIDVSN--NM 120
Db	21 SLHLVDSDSSLAK--VPD-----EAPK--VGIIGSGDFARSLATRLVGSGFKVWGSRN 60
Qy	71 PKRTARLIPSAAQVTFOEEEAVSSPEVIFVAVFREHYSSLCSSLSDQLAGKILVLDVSNPTEQ 130
Db	61 PKRTARLIPSAAQVTFOEEEAVSSPEVIFVAVFREHYSSLCSSLSDQLAGKILVLDVSNPTEQ 120
Qy	121 RINQYPPESNAEYLASLFPDSLIVKGFTNVSAWALQLGPKDASRQWYICSNNIQARQQVE 180
Db	131 EHLQHRESNAEYLASLFPCTCTVKAFTNVISAWTLOQAGPRDGNRQVPICGDQEAKRAVE 180
Qy	181 LAROLNFIPIDLGLSLSAREIENLPLRIFTLWRGPVVVAISLATFFFLYSFVRDVTHPYA 240
Db	191 MALAMGMPVDMGSLASAWEEVAMPLRILPAWKVPTILLALGLFVCFYAYNEFVRDVQPYV 250
Qy	241 RNQQSDFYKIPIEIWNKTLPIVAITLISLVLAGLLAAVQLYYGGTKYRREPPWLETWQ 300
Db	251 QESQNKFKKLPVSVVNTTLPVCVAVVILSLVILPGVLAALQLRRGTYQRFPDWLDHMLQ 310
Qy	301 CRKQLGILSFFPAMVHVAISLCLPMRMRSERVLFLINMAYQQVHANIENSWNEEVWRIEMY 360
Db	311 HRKOIGLILSFFCAALHALYSPCFCPLRRAHRYDVLNLAVKQVLANKSHLWEEEVWMEIY 370
Qy	361 ISFGIMMSLGLSLLAVTSIPSVSNALNREFSFIFIQSTLGVALLISTFHVLIVGWKRAFE 420
Db	371 LSLGVLAIGTLSLLAVTSLPSIANSLNWREFSFVQSSLGFVALVLSTLHTLTGWTAFE 430
Qy	421 EYYXRFYTPPNFVTLALVLPSIVL 444
Db	431 ESRYKFYLPPTFTLTLVPCVVL 454
RESULT 11	
PINVB5	PRELIMINARY; PRT; 488 AA.
Q9NVB5	PRELIMINARY; PRT; 488 AA.
Q9NVB5;	PRELIMINARY; PRT; 488 AA.
01-OCT-2000	(TREMBLrel. 15, Created)
01-OCT-2000	(TREMBLrel. 15, Last sequence update)
01-JUN-2003	(TREMBLrel. 24, Last annotation update)
Hypothetical protein	FIJ10829 (Dudulin 2).
Homologous	Homo sapiens (Human).
Eukaryota;	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;	NCBI_TAXID=9606;
[1]	
SEQUENCE FROM N.A.	
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshioka Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuko Y., Sasaki N.; "NEO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.	
[2]	
SEQUENCE FROM N.A.	
Serru V., Manivet P., Lenoir C., Eschwege P., Lamblin D., Vaubourdolle M., Kellermann O., Loric S.; "Dudulin 2, a new tumor antigen expressed in various human tumors."; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
EMBL; AK001691; BAA91839.1; -.	
EMBL; AY029585; AAK50538.1; -.	
GO; GO:0006118; P:electron transport; IEA.	
InterPro; IPR003006; Ig_MHC.	
InterPro; IPR004455; NADPoxred_F420.	
Pfam; PF03807; F420_oxidored; I.	
PROSITE; PS00290; Ig_MHC; 1.	
Hypothetical protein.	
SEQUENCE 488 AA; 54616 MW; BC0BCA483335AAD6 CRC64;	
Query Match	53.3%; Score 1252.5; DB 4; Length 487;
Best Local Similarity	54.1%; Pred. No. 1.6e-92;
Matches	240; Conservative 83; Mismatches 108; Indels 13; Gaps 5;
Indels	13; Gaps 5;
Qy	3 SISMMGSPKSLSETCLPNGINGIKDARKVTVGIGSGDFAKSLTIRLCGYHVWIGSRN 62
Db	11 SLHLVDSDSSLAK--VPD-----EAPKVS--ILGSGDFARSLATRLVGSGFKVWGSRN 60
Qy	63 PKFASEFFPHVVDVTTHEDALTKTNIIFVAIHRHEHTSLWDLRHLVGKILIDVSN--NM 120
Db	11 SLHLVDSDSSLAK--VPD-----EAPKVS--ILGSGDFARSLATRLVGSGFKVWGSRN 60
Qy	63 PKFASEFFPHVVDVTTHEDALTKTNIIFVAIHRHEHTSLWDLRHLVGKILIDVSN--NM 120
Db	11 SLHLVDSDSSLAK--VPD-----EAPKVS--ILGSGDFARSLATRLVGSGFKVWGSRN 60
Qy	121 RINQYPPESNAEYLASLFPDSLIVKGFTNVSAWALQLGPKDASRQWYICSNNIQARQQVE 180
Db	121 EHLQHRESNAEYLASLFPCTCTVKAFTNVISAWTLOQAGPRDGNRQVPICGDQEAKRAVE 180
Qy	181 LAROLNFIPIDLGLSLSAREIENLPLRIFTLWRGPVVVAISLATFFFLYSFVRDVTHPYA 240
Db	181 MALAMGMPVDMGSLASAWEEVAMPLRILPAWKVPTILLALGLFVCFYAYNEFVRDVQPYV 250
Qy	241 RNQQSDFYKIPIEIWNKTLPIVAITLISLVLAGLLAAVQLYYGGTKYRREPPWLETWQ 300
Db	241 QESQNKFKKLPVSVVNTTLPVCVAVVILSLVILPGVLAALQLRRGTYQRFPDWLDHMLQ 300
Qy	301 CRKQLGILSFFPAMVHVAISLCLPMRMRSERVLFLINMAYQQVHANIENSWNEEVWRIEMY 360
Db	301 HRKOIGLILSFFCAALHALYSPCFCPLRRAHRYDVLNLAVKQVLANKSHLWEEEVWMEIY 360
Qy	361 ISFGIMMSLGLSLLAVTSIPSVSNALNREFSFIFIQSTLGVALLISTFHVLIVGWKRAFE 420
Db	361 LSLGVLAIGTLSLLAVTSLPSIANSLNWREFSFVQSSLGFVALVLSTLHTLTGWTAFE 420
Qy	421 EYYXRFYTPPNFVTLALVLPSIVL 444
Db	421 ESRYKFYLPPTFTLTLVPCVVL 444
RESULT 12	
Q8NEW6	PRELIMINARY; PRT; 488 AA.
ID	Q8NEW6
AC	Q8NEW6;
DT	01-OCT-2002 (TREMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Phyde.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TAXID=9606;
RN	NCBI_TAXID=9606;
RP	SEQUENCE FROM N.A.
RA	Lu Y., Beheshti B., Squire J.A., Yang X.J.; "Characterization of a novel apoptosis-inducing gene, hphyde, that inhibits prostate cancer cell growth."; Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RT	EMBL; AY082673; AAC45136.1; -.
RT	GO; GO:0006118; P:electron transport; IEA.
RT	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR004455; NADPoxred_F420.
DR	Pfam; PF03807; F420_oxidored; I.
DR	PROSITE; PS00290; Ig_MHC; 1.
SQ	SEQUENCE 487 AA; 54501 MW; E0EF95E855C81EDF CRC64;
Query Match	53.3%; Score 1252.5; DB 4; Length 487;
Best Local Similarity	54.1%; Pred. No. 1.6e-92;
Matches	240; Conservative 83; Mismatches 108; Indels 13; Gaps 5;
Indels	13; Gaps 5;
Qy	3 SISMMGSPKSLSETCLPNGINGIKDARKVTVGIGSGDFAKSLTIRLCGYHVWIGSRN 62
Db	11 SLHLVDSDSSLAK--VPD-----EAPKVS--ILGSGDFARSLATRLVGSGFKVWGSRN 60

Query Match 53.0%; Score 1245.5; DB 4; Length 487;
 Best Local Similarity 53.8%; Pred. No. 5.8e-92; Mismatches 239; Conservative 83; Mismatches 109; Indels 13; Gaps 5;

Query Match 45.7%; Score 1074.5; DB 4; Length 456;
 Best Local Similarity 52.9%; Pred. No. 3.2e-78; Mismatches 209; Conservative 75; Mismatches 98; Indels 13; Gaps 5;

Query Match 3 SISMNGSPKSLSSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVVIGSRN 62
 11 SLHLVDSDSLAK--VFD----EAPKVS--IIGSGDFARSLATRLVGSGFKVVGSRN 60

Query Match 63 PKPASEFFPHVVDVTHEDALTNTIFVAIHREHYTSWLDRHLLVGKILIDVSN--NM 120
 61 PKRTARLFPSAAQVTQEEAVSSPEVIFAVAVEREHYSSLCSLSDQLAGKILVDVSNPTEQ 120

Query Match 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIQARQVIE 180
 121 EHLQHRESNAEYLASLFPCTVKAFAVNISAWTLQAGPRDGNGQVPCGDOPEAKRAVE 180

Query Match 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240
 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240

Query Match 181 MALAMGFMPPDMGSLASAWEVEMPLRLLPAWKVPTLALGLFVCFYAYNFVRDVHQPV 240
 181 MALAMGFMPPDMGSLASAWEVEMPLRLLPAWKVPTLALGLFVCFYAYNFVRDVHQPV 240

Db 61 PKRTARLFPSAAQVTQEEAVSSPEVIFAVAVEREHYSSLCSLSDQLAGKILVDVSNPTEQ 120
 121 EHLQHRESNAEYLASLFPCTVKAFAVNISAWTLQAGPRDGNGQVPCGDOPEAKRAVE 180
 181 MALAMGFMPPDMGSLASAWEVEMPLRLLPAWKVPTLALGLFVCFYAYNFVRDVHQPV 240
 Db 241 QESQNKEFKLPLPVSVNTLPCVAVTLISLVLPGTAALQRRGCKYQRFPDWLDHWLQ 300
 301 CRKQOLGILSFFPMRSERYLFLINMAYQOQHANTENSNEEEVWRIMY 360
 301 HRKOIGLISFFCPLRRAHYDLVNLAVKQVLANKSHLW-VEEVWRMEY 359
 361 ISFGIMSLGLLSSLAVTSIPSVSNALNWREFSFTOSTLGYVALISTFHVLIGWRAFE 420
 360 LSLGVLAIGLTLISLAVTSIANSLNWREFSFVQSSIGFVALVSTHTLTGWTRAFE 419
 421 EYYRFYTPPNFVLALVLPSITVL 444
 420 ESRYKFYLPPFTLILVPCVIL 443

RESULT 13

Q8TF03 PRELIMINARY; PRT; 487 AA.
 AC Q8TF03;
 DT 01-JUN-2002 (TiEMBLrel. 21, Created)
 DT 01-JUN-2002 (TiEMBLrel. 21, Last sequence update)
 DE 01-JUN-2003 (TiEMBLrel. 24, Last annotation update)
 PRYDE II.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang C., Alay J.A., Steiner M.S.;
 RT "Second human member of phyre family, Human phyre II."
 RL Submitted (May-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF262322; AAM08128.1; -.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR004455; NADPoxred_F420.
 DR Pfam; PF03807; F420 oxidored; T.
 DR PROSITE; PS00290; IG MHC; 1.
 DR SEQUENCE; PS00290; IG MHC; 1.
 DR SEQUENCE; 456 AA; 50430 MW; C5F7C7008D55251E CRC64;

Query Match 53.0%; Score 1245.5; DB 4; Length 487;
 Best Local Similarity 53.8%; Pred. No. 5.8e-92; Mismatches 239; Conservative 83; Mismatches 109; Indels 13; Gaps 5;

Query Match 45.7%; Score 1074.5; DB 4; Length 456;
 Best Local Similarity 52.9%; Pred. No. 3.2e-78; Mismatches 209; Conservative 75; Mismatches 98; Indels 13; Gaps 5;

Query Match 3 SISMNGSPKSLSSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVVIGSRN 62
 11 SLHLVDSDSLAK--VFD----EAPKVS--IIGSGDFARSLATRLVGSGFKVVGSRN 60

Query Match 63 PKPASEFFPHVVDVTHEDALTNTIFVAIHREHYTSWLDRHLLVGKILIDVSN--NM 120
 61 PKRTARLFPSAAQVTQEEAVSSPEVIFAVAVEREHYSSLCSLSDQLAGKILVDVSNPTEQ 120

Query Match 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIQARQVIE 180
 121 EHLQHRESNAEYLASLFPCTVKAFAVNISAWTLQAGPRDGNGQVPCGDOPEAKRAVE 180

Query Match 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240
 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240

Query Match 241 RNOQDFYKIPIEVNKTLPVAVITLSSLVLAGLLAAAYOLYGTKVRFPFWLETWLO 300
 241 QESQNKEFKLPLPVSVNTLPCVAVTLISLVLPGTAALQRRGCKYQRFPDWLDHWLQ 300
 301 CRKQOLGILSFFPMRSERYLFLINMAYQOQHANTENSNEEEVWRIMY 360
 301 HRKOIGLISFFCPLRRAHYDLVNLAVKQVLANKSHLW-VEEVWRMEY 359
 361 ISFGIMSLGLLSSLAVTSIPSVSNALNWREFSFTOSTLGYVALISTFHVLIGWRAFE 420
 360 LSLGVLAIGLTLISLAVTSIANSLNWREFSFVQSSIGFVALVSTHTLTGWTRAFE 419
 421 EYYRFYTPPNFVLALVLPSITVL 444
 420 ESRYKFYLPPFTLILVPCVIL 443

RESULT 14

Q8TDP3 PRELIMINARY; PRT; 456 AA.
 AC Q8TDP3;
 DT 01-JUN-2002 (TiEMBLrel. 21, Created)
 DT 01-JUN-2002 (TiEMBLrel. 21, Last sequence update)
 DE PRYDE II.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RA Wang C., Alay J.A., Steiner M.S.;
 RT "Second human member of phyre family, Human phyre II."
 RL Submitted (May-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF262322; AAM08128.1; -.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR004455; NADPoxred_F420.
 DR Pfam; PF03807; F420 oxidored; T.
 DR PROSITE; PS00290; IG MHC; 1.
 DR SEQUENCE; 456 AA; 50430 MW; C5F7C7008D55251E CRC64;

Query Match 53.0%; Score 1245.5; DB 4; Length 487;
 Best Local Similarity 53.8%; Pred. No. 5.8e-92; Mismatches 239; Conservative 83; Mismatches 109; Indels 13; Gaps 5;

Query Match 45.7%; Score 1074.5; DB 4; Length 456;
 Best Local Similarity 52.9%; Pred. No. 3.2e-78; Mismatches 209; Conservative 75; Mismatches 98; Indels 13; Gaps 5;

Query Match 3 SISMNGSPKSLSSETCLPNGINGIKDARKVTGVIGSGDFAKSLTIRLIRCGYHVVIGSRN 62
 11 SLHLVDSDSLAK--VFD----EAPKVS--IIGSGDFARSLATRLVGSGFKVVGSRN 60

Query Match 63 PKPASEFFPHVVDVTHEDALTNTIFVAIHREHYTSWLDRHLLVGKILIDVSN--NM 120
 61 PKRTARLFPSAAQVTQEEAVSSPEVIFAVAVEREHYSSLCSLSDQLAGKILVDVSNPTEQ 120

Query Match 121 RINQYPESNAEYLASLFPDSLIVKGPNVSAWALQLGPKDASRQVTCNSNIQARQVIE 180
 121 EHLQHRESNAEYLASLFPCTVKAFAVNISAWTLQAGPRDGNGQVPCGDOPEAKRAVE 180

Query Match 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240
 181 LARQINFIPIDLGSLSSAREIENPLRLFTLWRGPVVAISLATFFLYSFVRDVHPIA 240

Query Match 241 RNOQDFYKIPIEVNKTLPVAVITLSSLVLAGLLAAAYOLYGTKVRFPFWLETWLO 300
 241 QESQNKEFKLPLPVSVNTLPCVAVTLISLVLPGTAALQRRGCKYQRFPDWLDHWLQ 300
 301 CRKQOLGILSFFPMRSERYLFLINMAYQOQHANTENSNEEEVWRIMY 360
 301 HRKOIGLISFFCPLRRAHYDLVNLAVKQVLANKSHLW-VEEVWRMEY 359
 360 LSLGVLAIGLTLISLAVTSIANSLNWREFSFVQ 394

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Job time : 89 secs